



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179469

TO: Delia Ramirez
Location: 2d74 / 2c70
Art Unit: 1652
Friday, February 17, 2006

Case Serial Number: 10/040018

From: Noble Jarrell
Location: Biotech-Chem Library
Rem 1B71
Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes

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Jarrell, Noble

179469

From: Ramirez, Delia
Sent: Monday, February 13, 2006 10:22 AM
To: Jarrell, Noble
Subject: 10/041018

Hi,

I would like to request the following *interference* search:

1. SEQ ID NO: 1, 361, 22 and 383 in the nucleic acid databases.
2. nucleotides 10000-10200 of SEQ ID NO:399 in the nucleic acid databases.

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

Mtbe
Fin 2/17/06
SNA
Compuer SPR
Soul

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 06:38:14 ; Search time 145.397 Seconds
(without alignments)
2934.525 Million cell updates/sec

Title: US-10-041-018-399_COPY_10000_10200

Perfect score: 201

Sequence: 1 aagaagtagcacattcataa.....catcgctattgcactctgca 201

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:

- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32.6	16.2	187745	12	US-11-121-086-83
2	31.2	15.5	581	6	US-09-925-065A-194717
3	31.2	15.5	613	6	US-09-925-065A-114512
4	30.8	15.3	581	6	US-09-925-065A-114514
5	30.8	15.3	613	6	US-09-925-065A-114513
c 6	30.8	15.3	638	6	US-09-925-065A-54797
c 7	30.4	15.1	583	6	US-09-925-065A-446887
c 8	30.2	15.0	458	6	US-09-925-065A-146565
9	30.2	15.0	520	6	US-09-925-065A-22533
10	30.2	15.0	520	6	US-09-925-065A-22534
c 11	30.2	15.0	2072	6	US-09-925-065A-700722
c 12	30.2	15.0	2072	6	US-09-925-065A-700723
c 13	30.2	15.0	2072	6	US-09-925-065A-700724
c 14	30.2	15.0	2072	6	US-09-925-065A-700725
15	30.2	15.0	2722	8	US-10-750-185-25210
16	30.2	15.0	2722	8	US-10-750-185-25210
c 17	30	14.9	574	6	US-09-925-065A-195489
c 18	30	14.9	638	6	US-09-925-065A-197353
c 19	29.8	14.8	600	12	US-11-136-527-4276
c 20	29.8	14.8	2505	8	US-10-750-185-26139

c 21	29.8	14.8	2505	8	US-10-750-623-26139
c 22	29.8	14.8	2519	12	US-11-136-527-180
c 23	29.6	14.7	913	8	US-10-750-185-38221
c 24	29.6	14.7	913	8	US-10-750-623-38221
c 25	29.4	14.6	527	6	US-09-925-065A-437898
c 26	29.4	14.6	919	8	US-10-750-185-49248
c 27	29.4	14.6	919	8	US-10-750-623-49248
c 28	29.4	14.6	1137	8	US-10-750-185-35492
c 29	29.4	14.6	1137	8	US-10-750-623-35492
c 30	29.4	14.6	18682	12	US-11-112-908-23
c 31	29.2	14.5	604	6	US-09-925-065A-210001
c 32	29	14.4	600	8	US-10-750-185-20355
c 33	29	14.4	600	8	US-10-750-623-20355
c 34	29	14.4	1027	8	US-10-750-185-38774
c 35	29	14.4	1027	8	US-10-750-623-38774
c 36	29	14.4	2681	12	US-11-239-325-8
c 37	29	14.4	2699	12	US-11-239-325-26
c 38	29	14.4	319608	12	US-11-145-703-1
c 39	28.8	14.3	545	6	US-09-925-065A-24019
c 40	28.8	14.3	578	6	US-09-925-065A-379132
c 41	28.8	14.3	599	6	US-09-925-065A-634390
c 42	28.8	14.3	915	8	US-10-750-185-46586
c 43	28.8	14.3	915	8	US-10-750-623-46586
c 44	28.6	14.2	645	6	US-09-925-065A-165968
c 45	28.4	14.1	578	6	US-09-925-065A-379130

ALIGNMENTS

RESULT 1

US-11-121-086-83
; Sequence 83, Application US/11121086
; Publication No. US20050286459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 83
; LENGTH: 187745
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-83

Query Match 16.2%; Score 32.6; DB 12; Length 187745;
Best Local Similarity 60.9%; Pred. No. 9.7;
Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy	8	AGCACATTCATACGAAGAGTACGAACCTGTTACACCCCGAGACAGTTGCCCTA	67
Db	53154	AGGCAGATCAACATCGGAGATACAAACTGTTCAAGTACTCATACACTGTTCCATTA	53213
Qy	68	TATCGCTTTTCCCTATCAATAGTTTCT	94
Db	53214	TATCCCTATCCCAATCCATTACTCT	53240

RESULT 2

US-09-925-065A-194717
; Sequence 194717, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135

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; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194717
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-194717

Query Match      15.5%; Score 31.2; DB 6; Length 581;
Best Local Similarity 57.0%; Pred. No. 4.6;
Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTCCTTATATCGCTTTCCCTATCAATAGTTCTAA 96
DB 275 CATCCTTAAACTTCCTGCGCTGATGCTCTTGTGCGATCTGTTGATTATAGATCCCAA 334

QY 97 CTCATGTCAGTCTTGGGATCACAACTCCTTCAGTTGTAC 136
DB 335 GTCCTCCCTTTCTTTGTAATACATCCTCATCTGTTCTGC 374

RESULT 3
US-09-925-065A-114512
; Sequence 114512, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114512
; LENGTH: 613
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-114512

Query Match      15.5%; Score 31.2; DB 6; Length 613;
Best Local Similarity 57.0%; Pred. No. 4.7;
Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTCCTTATATCGCTTTCCCTATCAATAGTTCTAA 96
DB 367 CATCCTTAAACTTCCTGCGCTGATGCTCTTGTGCGATCTGTTGATTATAGATCCCAA 426

QY 97 CTCATGTCAGTCTTGGGATCACAACTCCTTCAGTTGTAC 136
DB 427 GTCCTCCCTTTCTTTGTAATACATCCTCATCTGTTCTGC 466

; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114513
; LENGTH: 613
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-114513

Query Match      15.3%; Score 30.8; DB 6; Length 581;
Best Local Similarity 56.0%; Pred. No. 6.2;
Matches 56; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTCCTTATATCGCTTTCCCTATCAATAGTTCTAA 96
DB 275 CATCCTTAAACTTCCTGCGCTGATGCTCTTGTGCGATCTGTTGATTATAGATCCCAA 334

QY 97 CTCATGTCAGTCTTGGGATCACAACTCCTTCAGTTGTAC 136
DB 335 GTCCTCCCTTTCTTTGTAATACATCCTCATCTGTTCTGC 374

RESULT 5
US-09-925-065A-114513
; Sequence 114513, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114513
; LENGTH: 613
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-114513
```

Query Match 15.3%; Score 30.8; DB 6; Length 613;
Best Local Similarity 56.0%; Pred. No. 6.3;
Matches 56; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTCCTTATATCGTTTTCCTATCAATAGTTTCTAA 96
DB 367 CATCCCTTAAACTTCCCTGGCGCTGATGTCCTTTGTCRGATCTGTGATTTATAGATCCCA 426

QY 97 CTCATGTCAGTCTTGCATCACAACTCCCTTCAGTTGTAC 136
DB 427 GTCTTCTCTTCTTGTGTAATACATCCTCATTCGTCTGTC 466

RESULT 6

US-09-925-065A-54797/c
; Sequence 54797, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54797
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-54797

Query Match 15.3%; Score 30.8; DB 6; Length 638;
Best Local Similarity 57.1%; Pred. No. 6.4;
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 66 TATATCGTTTCCCTATCAATAGTTTCTAACTCATGTCAGTCTTGGATCAACCTCC 125
DB 627 TCTGTAGATATTACTCATGTAGTGTGAGAAAATCATCCAGTCATGCCACATTTCTCC 568

QY 126 TTCAGTTGTACCGCTACATCTGACAACTCCACAGTC 163
DB 567 TTCCCATGATCTGCTAGTTTGCAACATATTCAGGTC 530

RESULT 7

US-09-925-065A-446887
; Sequence 446887, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 446887
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-446887

Query Match 15.1%; Score 30.4; DB 6; Length 583;
Best Local Similarity 63.9%; Pred. No. 8.3;
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTCCTTATATCGTTTTCCTATCAATAGTTTCTAA 96
DB 135 CCTCATTAATCTCTTCCAAGAGAGCTTCCCTGTCTCGGTTTGGCATATCTCTCT 194

QY 97 CTCATGTCAGTC 108
DB 195 TTCATGTGGGTC 206

RESULT 8

US-09-925-065A-146565/c
; Sequence 146565, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146565
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-146565

Query Match 15.0%; Score 30.2; DB 6; Length 458;
Best Local Similarity 60.2%; Pred. No. 8.9;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 14 TTCATAAGCAAGAGAGTAGCAAACTGTTTACACCCCGAGACAGTTCCTATATCGC 73
DB 214 TTGATGATGAAAAGTAGAATGCTAACTGATTGCACACAGTGCCTTACATACATAGA 155

QY 74 TTTTCCCTATCAATAGTTTCTAA 96
DB 154 TTAATCTATTATTGTTGCTAA 132

RESULT 9

US-09-925-065A-22533
; Sequence 22533, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single

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; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22533
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-22533

Query Match      15.0%; Score 30.2; DB 6; Length 520;
Best Local Similarity 58.2%; Pred. No. 9.3;
Matches 53; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 50 CCCGACAGATGGCCCTATATCGCTTTTCCCTATCAATAGTTTCTCAACTCATGTGTCAGTCT 109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 CCTGACACAGCGCCAGTGTTCCTATGCTCATCAATATTATTTCTTTGTTGCTGGAT 233

QY 110 TCGGATCACAACTCTTCAGTTGTACCGCT 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 234 CGTGCTTGTAACCTCTCAAGGTGTCTCCT 264

RESULT 10
US-09-925-065A-22534
; Sequence 22534, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22534
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-22534

Query Match      15.0%; Score 30.2; DB 6; Length 520;
Best Local Similarity 58.2%; Pred. No. 9.3;
Matches 53; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 50 CCCGACAGATGGCCCTATATCGCTTTTCCCTATCAATAGTTTCTCAACTCATGTGTCAGTCT 109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 CCTGACACAGCGCCAGTGTTCCTATGCTCATCAATATTATTTCTTTGTTGCTGGAT 233

QY 110 TCGGATCACAACTCTTCAGTTGTACCGCT 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 234 CGTGCTTGTAACCTCTCAAGGTGTCTCCT 264

RESULT 11
US-09-925-065A-700722/c
; Sequence 700722, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 700722
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-700722

Query Match      15.0%; Score 30.2; DB 6; Length 2072;
Best Local Similarity 60.2%; Pred. No. 14;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 14 TTCATAAGCAGAGAGTAGGAAACCTGTTACACCCCGACAGACAGTTGCCCTATATCCG 73
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 951 TTGATGATGAAAGTGAATGCTTAAGTGCACACACCGTGCCCGCATACCTTACATAGA 892

QY 74 TTTTCCCTATCAATAGTTTCTAA 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 891 TTAUCTTATTATTAATTGTTGCTTAA 869

RESULT 12
US-09-925-065A-700723/c
; Sequence 700723, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 700723
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-700723
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Search completed: February 16, 2006, 13:52:14
Job time : 146.397 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 05:56:03 ; Search time 34.8071 Seconds
(without alignments)
10264.856 Million cell updates/sec

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Sequence: 1 agaaagtagcacattcataa.....catcgctattgcactctgca 201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	102	50.7	2340	US-09-614-221A-299	Sequence 299, App
2	35.2	17.5	5622	US-09-067-800-3	Sequence 3, Appli
3	35.2	17.5	5622	US-09-349-677-3	Sequence 3, Appli
4	32	15.9	4953	US-09-620-312D-240	Sequence 240, App
5	31.6	15.7	1914	US-09-489-039A-2072	Sequence 2072, Ap
6	31.4	15.6	28932	US-09-949-016-16653	Sequence 16653, A
7	31	15.4	5583	US-09-312-283C-372	Sequence 372, App
8	30.8	15.3	1797	US-09-248-796A-5087	Sequence 5087, Ap
9	30.4	15.1	642	US-09-533-559-6096	Sequence 6096, Ap
10	30.2	15.0	128516	US-09-949-016-13501	Sequence 13501, A
11	30.2	15.0	133157	US-09-949-016-12541	Sequence 12541, A
12	30	14.9	69263	US-09-949-016-12594	Sequence 12594, A
13	30	14.9	69709	US-09-949-016-16036	Sequence 16036, A
14	29.8	14.8	390416	US-09-949-016-16923	Sequence 16923, A
15	29.6	14.7	832	US-09-621-976-2813	Sequence 2813, Ap
16	29.6	14.7	2508	US-09-949-016-1466	Sequence 1466, Ap
17	29.6	14.7	97989	US-09-949-016-13208	Sequence 13208, A
18	29.4	14.6	896	US-09-067-800-5	Sequence 5, Appli
19	29.4	14.6	896	US-09-349-677-5	Sequence 5, Appli
20	29.4	14.6	896	US-09-981-087A-3	Sequence 3, Appli
21	29.4	14.6	896	US-09-978-382A-3	Sequence 3, Appli
22	29.4	14.6	896	US-09-978-740A-3	Sequence 3, Appli
23	29.4	14.6	896	US-09-978-729A-3	Sequence 3, Appli
24	29.4	14.6	896	US-09-978-730-3	Sequence 3, Appli

C 25	29.4	14.6	1213	2	US-08-554-612C-14	Sequence 14, Appl
C 26	29.4	14.6	95318	3	US-09-949-016-11784	Sequence 11784, A
C 27	29.4	14.6	95318	3	US-09-949-016-13998	Sequence 13998, A
C 28	29.2	14.5	601	3	US-09-949-016-64625	Sequence 64625, A
C 29	29.2	14.5	36311	3	US-09-949-016-13627	Sequence 13627, A
C 30	29	14.4	319608	3	US-09-539-333D-1	Sequence 1, Appli
C 31	29	14.4	319608	3	US-09-679-409-1	Sequence 1, Appli
C 32	28.8	14.3	7813	3	US-09-573-080A-27	Sequence 27, Appli
C 33	28.6	14.2	1308	3	US-09-489-039A-116	Sequence 116, App
C 34	28.6	14.2	171700	3	US-09-949-016-12276	Sequence 12276, A
C 35	28.6	14.2	171701	3	US-09-949-016-15835	Sequence 15835, A
C 36	28.4	14.1	10718	3	US-09-949-016-11918	Sequence 11918, A
C 37	28.4	14.1	10718	3	US-09-949-016-13816	Sequence 13816, A
C 38	28.2	14.0	1521	2	US-08-670-354-3	Sequence 3, Appli
C 39	28.2	14.0	1521	3	US-09-320-424-3	Sequence 3, Appli
C 40	28.2	14.0	1521	3	US-09-825-563-3	Sequence 3, Appli
C 41	28.2	14.0	1521	6	PCT-US96-10895-3	Sequence 3, Appli
C 42	28.2	14.0	1606	3	US-09-919-039-117	Sequence 117, App
C 43	28.2	14.0	1711	3	US-09-569-611C-15	Sequence 15, Appli
C 44	28.2	14.0	1751	2	US-08-670-354-1	Sequence 1, Appli
C 45	28.2	14.0	1751	3	US-09-320-424-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-614-221A-299
; Sequence 299, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanadaa, Balasulojini
; APPLICANT: Yu, Jaehyuk
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614,221A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 299
; LENGTH: 2340
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-299

Query Match 50.7%; Score 102; DB 3; Length 2340;
Best Local Similarity 100.0%; Pred. No. 3.5e-25;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 100 ATGTGAGTCTTGGATCACAACCTCTTCAGTTGTACCGCTACATCTGCAACATCCACC 159
DB 1 ATGTGAGTCTTGGATCACAACCTCTTCAGTTGTACCGCTACATCTGCAACATCCACC 60
QY 160 AGTCGCAAAACAGAACAGGACCATCGCTATTGCACTCTGCA 201
DB 61 AGTCGCAAAACAGAACAGGACCATCGCTATTGCACTCTGCA 102

RESULT 2
US-09-067-800-3/c
; Sequence 3, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP

```

; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..5622
; OTHER INFORMATION: /label= AGL1_promoter
; US-09-067-800-3
; OTHER INFORMATION: /note= "Nucleotide sequence of the AGL1 promoter."

Query Match          17.5%; Score 35.2; DB 3; Length 5622;
Best Local Similarity 58.7%; Pred. No. 0.077; 43; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 0;

QY 66 TATATCGCTTTTCCCTATCAATAGTTTCTTAATCTAGTCAGTCTTGGCATCACACCTCC 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2674 TATCTATTATTTCCCTCTCCCTAGTTTCTTGCTACTCTCTGCGTGTGACTACTCCACC 2615
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 126 TTCAGTTGTACGGTACATCTGACACATCCACCATCCGACGTCGCAAAA 169
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2614 TTCCTCCATTGATCATATATGACATCATCCAAATAATTAATAAA 2571
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 3
US-09-349-677-3/c
; Sequence 3, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Vanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:

; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..5622
; OTHER INFORMATION: /label= AGL1_promoter
; US-09-067-800-3
; OTHER INFORMATION: /note= "Nucleotide sequence of the AGL1 promoter."

Query Match          17.5%; Score 35.2; DB 3; Length 5622;
Best Local Similarity 58.7%; Pred. No. 0.077; 43; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 0;

QY 66 TATATCGCTTTTCCCTATCAATAGTTTCTTAATCTAGTCAGTCTTGGCATCACACCTCC 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2674 TATCTATTATTTCCCTCTCCCTAGTTTCTTGCTACTCTCTGCGTGTGACTACTCCACC 2615
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 126 TTCAGTTGTACGGTACATCTGACACATCCACCATCCGACGTCGCAAAA 169
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2614 TTCCTCCATTGATCATATATGACATCATCCAAATAATTAATAAA 2571
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
US-09-620-312D-240/c
; Sequence 240, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 240
; LENGTH: 4953
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4953)
US-09-620-312D-240

Query Match      15.9%; Score 32; DB 3; Length 4953;
Best Local Similarity 65.3%; Pred. No. 0.95;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 37 CCTGTTTACACCCCGAGAGAGTGGCCCTATATCGCTTTCCCTATCAATAGTTCTTAA 96
Db 819 CCYCTTTAACTTCCAGAGAGCTTCCCTGTATCGGTTTGGCCCTTATGCTCTCT 760
Qy 97 CTCATGTCAGTC 108
Db 759 TTCATTGGGTC 748

RESULT 5
US-09-489-039A-2072
; Sequence 2072, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2072
; LENGTH: 1914
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1300), (1329)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-489-039A-2072

Query Match      15.7%; Score 31.6; DB 3; Length 1914;
Best Local Similarity 60.5%; Pred. No. 0.92;
Matches 52; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 18 TAGCAGAGAGTACGAACTGTTTACACCCCGAGAGAGTGGCCCTATATCGCTTTT 77
Db 122 TAAACAGCGCGTGGCGGAAACGGTATAATCGAGCGGAAAAAACCACGATATAGCGTTT 181
Qy 78 CCTATCAATAGTTCTTAATCATGT 103
Db 182 CGCGTGCATTAATTTATACATATT 207

RESULT 6
US-09-949-016-16653/c
; Sequence 16653, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 16653
; LENGTH: 28932
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16653

Query Match      15.6%; Score 31.4; DB 3; Length 28932;
Best Local Similarity 50.3%; Pred. No. 3;
Matches 77; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 24 AGAGAGTACGAAACCTGTTTACACCCCGAGAGAGTGGCCCTATATCGCTTTTCCCTAT 83
Db 27038 AAAAAGTGCTAAACATATTTACAGCAATGTGCTAAGTGAAGCTCTGAGTTAAATTCAGAT 26979
Qy 84 CAATAGTTTCTTAATCTATGTCAGTCTTGGCATCACACCTCTCTTACGCTTACCGCTACA 143
Db 26978 CTAGACAAAAAATCTGAGGCTTAAGCTTTATGTACAAACAAGTTTACAAGTCCCTCCACA 26919
Qy 144 TCTGACAAACATCCACCAGTCGCAAAACAGAAACA 176
Db 26918 TATCAATACATAGGCATTACAGAACCAACA 26886

RESULT 7
US-09-312-283C-372
; Sequence 372, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 5583
; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283C-372

Query Match      15.4%; Score 31; DB 3; Length 5583;
Best Local Similarity 50.3%; Pred. No. 2.2;
Matches 76; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 24 AGAGAGTACGAAACCTGTTTACACCCCGAGAGAGTGGCCCTATATCGCTTTTCCCTAT 83
Db 601 AGAGCGGAGGAAAGACGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
Qy 84 CAATAGTTTCTTAATCTATGTCAGTCTTGGCATCACACCTCTCTTACGCTTACCGCTACA 143
Db 661 TACTGTGTGAGCATCTCTCCGGGTGCTGTGGGCTGCAAGACCGCCGAGAACTGGGCC 720
Qy 144 TCTGACAAACATCCACCAGTCGCAAAACAGAA 174
Db 721 TCGACACCGTCCACCTTTTACGCCAACCGAA 751

RESULT 8
US-09-248-796A-5087
; Sequence 5087, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
```


RESULT 12
US-09-949-016-12594
; Sequence 12594, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12594
; LENGTH: 69263
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(69263)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12594

Query Match 14.9%; Score 30; DB 3; Length 69263;
Best Local Similarity 54.5%; Pred. No. 13;
Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 59 GTTGCCCTATATCGCTTTCCCTATCAATGTTCTTAACATCAATGTCAGTCTTGGATCAC 118
DB 53870 GTCTCACTATGTGGTTTGGCCGCTCTCTAAGTCTTCAAGTGATCTCTCGCTC 53929

QY 119 AACTCTCTTCACTGTTGACGCTACATCTGACAAACATCCACAGTCGCAAA 168
DB 53930 AGCTTCCAAAGTTGTGGGATTACAGGTGTGAACACTACCACCTGTCCCAA 53979

US-09-949-016-16036
; Sequence 16036, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16036
; LENGTH: 69709
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(69709)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16036

Query Match 14.9%; Score 30; DB 3; Length 69709;
Best Local Similarity 54.5%; Pred. No. 13;

Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 59 GTTGCCCTATATCGCTTTCCCTATCAATGTTCTTAACATCAATGTCAGTCTTGGATCAC 118
DB 53870 GTCTCACTATGTGGTTTGGCCGCTCTCTAAGTCTTCAAGTGATCTCTCGCTC 53929

QY 119 AACTCTCTTCACTGTTGACGCTACATCTGACAAACATCCACAGTCGCAAA 168
DB 53930 AGCTTCCAAAGTTGTGGGATTACAGGTGTGAACACTACCACCTGTCCCAA 53979

RESULT 14
US-09-949-016-16923
; Sequence 16923, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16923
; LENGTH: 390416
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16923

Query Match 14.8%; Score 29.8; DB 3; Length 390416;
Best Local Similarity 54.0%; Pred. No. 29;
Matches 61; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 86 ATAGTTTCTAATCACTGTCAGTCTTGGATCAACCTCTTCAAGTCTTGGGAGACACC 145
DB 194856 ATAGTTTAGTCTCTCAGGGAACAATTTTATTTCATTATTCCTAAGTCTTGGGAGACACC 194915

QY 146 TGACAAATCCACAGTCGCAAAACAGACAGGAAACATCGCTATTGCACTCT 198
DB 194916 TTATGTATCCAAAGACTAACAACACCATCAGAGTGCAAAATCACTCT 194968

RESULT 15
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match 14.7%; Score 29.6; DB 3; Length 832;

Best Local Similarity 15.6%; Pred. No. 3.3;
Matches 29; Conservative 88; Mismatches 67; Indels 2; Gaps 1;

Qy	6	GTAGCACATTTCATAAGACAGAGTAGACGAAACCTGTTTACACCCCGGAGACAGATTGCCC	65
Db	70	KKAMCHTKTKKKKKGGYMMWYWGWRSSYMAWTRITWTCGYAYRSMMYWRRCWKKKAY	129
Qy	66	TATATCGCTTTTCCCTATCAATAGTTTCTAACTCATGTTCAGTTCGCGATCAACCTCC	125
Db	130	YRKTCYSSKGTWTKRWKKAWTTWKKTYTAAATRYWMMCW--KWRASWNYCWMM	187
Qy	126	TTCAGTTGTACCGCTACATCTGACAAATCCACCGTCCGAAACAGACAGAACCCATC	185
Db	188	GKARKWSTWRKRSYASARSKRCCYSCSWGAMSWKYMWRMRWRGWTGAGMKAWRASC	247
Qy	186	GCTATT	191
Db	248	MMRRKY	253

Search completed: February 16, 2006, 06:09:53
Job time : 36.8071 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 06:36:26 ; Search time 173.375 Seconds
(without alignments)
9587.015 Million cell updates/sec

Title: US-10-041-018-399_COPY_10000_10200

Perfect score: 201

Sequence: 1 aagaagtagcacattcataa.....catcgctattgcactctgca 201

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_Main:

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:
- 3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:
- 4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:
- 5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:
- 6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:
- 7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:
- 8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:
- 9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:
- 10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	201	100.0	39827	7	US-10-041-018-399
2	102	50.7	2340	8	US-10-793-639-299
3	35.2	17.5	5622	9	US-10-871-651A-5
4	32	15.9	657	3	US-09-864-761-20243
5	32	15.9	1216	9	US-10-450-763-7959
6	32	15.9	1367	9	US-10-450-763-27115
7	32	15.9	1857	9	US-10-450-763-8929
8	32	15.9	1976	3	US-09-864-761-3473
9	32	15.9	2365	9	US-10-450-763-8921
10	32	15.9	3118	9	US-10-450-763-6475
11	32	15.9	4953	5	US-10-037-270-240
12	32	15.9	4953	6	US-10-117-722-240
13	32	15.9	4953	9	US-10-450-763-6466
14	32	15.9	4953	9	US-10-450-763-27114
15	32	15.9	4953	9	US-10-122-851-240
16	32	15.9	5861	3	US-09-814-353-21084
17	32	15.9	87731	5	US-10-087-192-1342
18	31.6	15.7	3683	8	US-10-473-126-194
19	31.2	15.5	581	4	US-09-925-065A-194717
20	31.2	15.5	613	4	US-09-925-065A-114512
21	31.2	15.5	21537	6	US-10-311-455-1972
22	31	15.4	661	6	US-10-029-386-22736
23	31	15.4	3345	5	US-10-027-632-112866

ALIGNMENTS

RESULT 1

US-10-041-018-399
; Sequence 399, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P020800US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 399
; LENGTH: 39827
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-041-018-399

Query Match 100.0%; Score 201; DB 7; Length 39827;
Best Local Similarity 100.0%; Pred. No. 1.6e-57;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAAGTAGCACATTCAATAGCAAGAGAGTAGCAAAACCTGTTTACACCCCGAGACAGT 60
Db 10000 AGAAGTAGCACATTCAATAGCAAGAGAGTAGCAAAACCTGTTTACACCCCGAGACAGT 10059
QY 61 TGGCCTATATCGTGTTCCTTCAATATCTTCTTACTCATGTCAGTCTTGGCATCAAA 120
Db 10060 TGGCCTATATCGTGTTCCTTCAATATCTTCTTACTCATGTCAGTCTTGGCATCAAA 10119
QY 121 CTTCTTCTAGTTTGTACCGGTACATCTGCAAAACATCCACAGTCGCAAAACAGAACAGGAA 180
Db 10120 CTTCTTCTAGTTTGTACCGGTACATCTGCAAAACATCCACAGTCGCAAAACAGAACAGGAA 10179
QY 181 CCATCGCTATTGCACTCTGCA 201
Db 10180 CCATCGCTATTGCACTCTGCA 10200

RESULT 2

US-10-793-639-299
; Sequence 299, Application US/10793639
; Publication No. US20040199940A1

```

; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/10/793,639
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US/09/614,221A
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 299
; LENGTH: 2340
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-793-639-299

Query Match          50.7%; Score 102; DB 8; Length 2340;
Best Local Similarity 100.0%; Pred. No. 4.9e-24;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 ATGTGAGTCTTGGGATCAACCTCTTCAAGTTGTACCGCTATCATCTGACAAATCCACC 159
DB 1 ATGTGAGTCTTGGGATCAACCTCTTCAAGTTGTACCGCTATCATCTGACAAATCCACC 60

QY 160 AGTCGCAAAACAGAACAGGACCATCGCTATTGCACTCTGCA 201
DB 61 AGTCGCAAAACAGAACAGGACCATCGCTATTGCACTCTGCA 102

RESULT 3
US-10-871-651A-5/c
; Sequence 5, Application US/10871651A
; Publication No. US20050120417A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljgren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Control of Fruit Dehiscence in Arabidopsis by
; TITLE OF INVENTION: Indehiscent1 Genes
; FILE REFERENCE: 19452A-00071005
; CURRENT APPLICATION NUMBER: US/10/871,651A
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/548,971
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5622
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; OTHER INFORMATION: SHATTERPROOF1 (SHP1) genomic sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (935)..(941)
; OTHER INFORMATION: n = g, a, c or t
US-10-871-651A-5

Query Match          17.5%; Score 35.2; DB 9; Length 5622;
Best Local Similarity 58.7%; Pred. No. 0.58;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 66 TATATCGCTTTCCCTATCAATAGTTCTTAACATCATGTGCTGAGTCTTCCGATCAACCTCC 125
DB 2674 TATCTCTATTTTCCCTCTCCCTAGTTCTTGCTACTCTCTGCGTGTGACTACTCCACC 2615

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QY 126 TTCAGTTGTACCGCTATCATCTGACAAATCCACCATCCAGTCGCAAAA 169
DB 2614 TTCTCCATTGATCCATATATGACATCATCCAAATAATTAATAA 2571

RESULT 4
US-09-864-761-20243
; Sequence 20243, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20243
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL023280.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EST_HUMAN HIT: AW867015.1, EVALUATE 1.00e-124

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; OTHER INFORMATION: NT HIT: M10976.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P10262, EVALUE 3.00e-30
US-09-864-761-20243

```

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Query Match      15.9%; Score 32; DB 3; Length 657;
Best Local Similarity 65.3%; Pred. No. 3.1;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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[illegible]

Qy 97 CTCATGTCAGTC 108
|||||
Db 527 TTCATTGGGTC 538

RESULT 5
US-10-450-763-7959/c
; Sequence 7959, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

```

, FILE REFERENCE: 790CIP3/US
, CURRENT APPLICATION NUMBER: US/10/450,763
, CURRENT FILING DATE: 2003-06-11
, PRIOR APPLICATION NUMBER: PCT/US01/08631
, PRIOR FILING DATE: 2001-03-30
, PRIOR APPLICATION NUMBER: 09/540,217
, PRIOR FILING DATE: 2000-03-31
, PRIOR APPLICATION NUMBER: 09/649,167
, PRIOR FILING DATE: 2000-08-23
, NUMBER OF SEQ ID NOS: 60736
, SOFTWARE: Custom
, SEQ ID NO: 7959
, LENGTH: 1216
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, NAME/KEY: SIMILAR
, LOCATION: (151)..(1143)
, OTHER INFORMATION: 39% homologous to Fowlpox virus gag, accession number
, OTHER INFORMATION: AF006065, Smith-Waterman Score=556.
US-10-450-763-7959

```

```
Query Match      15.9%; Score 32; DB 9; Length 1216;
Best Local Similarity 65.3%; Pred. No. 4;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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Qy 37 CCTGTTTACACCCCCCGAGACAGTTGCCCTATATCGCTTTTCCCTATCAATAGTTCTAA 96
||| ||| | | | | | | | | | | | | | | | |
Db 669 CCTCTTTAATCCTTCCAAGAGAGCTTCCCTGTATCGTTTTAGCTTTTGCATATCCTCTCT 610

Qy 97 CTCATGTCAGTC 108
|||||
Db 609 TTCATTGGGTC 598

RESULT 6
US-10-450-763-27115
; Sequence 27115, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hvsseg. Inc

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1 FILE OF INVENTION: NOVEL NUCLEIC ACIDS
2
3 FILE REFERENCE: 790CI3/US
4
5 CURRENT APPLICATION NUMBER: US/10/450,763
6
7 CURRENT FILING DATE: 2003-06-11
8
9 PRIOR APPLICATION NUMBER: PCT/US01/08631
10
11 PRIOR FILING DATE: 2001-03-30
12
13 PRIOR APPLICATION NUMBER: 09/540,217
14
15 PRIOR FILING DATE: 2000-03-31

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; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 27115
; LENGTH: 1367
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1066)..(74)
; OTHER INFORMATION: 39%
; OTHER INFORMATION: AFO
US-10-450-763-27115

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Query Match      15.9%; Score 32; DB 9; Length 1367;
Best Local Similarity 65.3%; Pred. No. 4.1;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy 37 CCTGTTTACACCCCGAGACAGTTGCCCTATATCGCTTTTCCCCTATCAATAGTTCTTA 96
||| |||| | | | | | | | | | | | | | | | |
Db 548 CCTCTTTAATCTTTCCAAGAGCTTCCGTATCGGTATTCGGTTTTASCCTTGCATATCCTCTCT 60
||| |||| | | | | | | | | | | | | | | | |

Qy 97 CTCATGTCAGTC 108
Db 608 TTCATTTGGGTC 619

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RESULT 7
US-10-450-763-8929/c
; Sequence 8929, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790C1P3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 8929
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (800)..(1792)
; OTHER INFORMATION: 39% homologous to Fowlpox virus gag,
; OTHER INFORMATION: AF006065,Smith-Waterman Score=556.
US-10-450-763-8929

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Query Match      15.9%; Score 32; DB 9; Length 1857;
Best Local Similarity 65.3%; Pred. No. 4.7;
Matches 47: Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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Qy	37	CCTGTTTACACCCCCGAGACAGTTCGCCCTATATCGCTTTTCCCTATCAATAGTTTCTAA	96
Dδ	1318	CCTCTTTTAATCCTTCCAAGAGAGCTTCCCTGTATCGTTTAGCCTTTGCATATCCCTCTCT	1259
Qy	97	CTCATGTCAGTC	108
Dδ	1258	TTCATTGGGTC	1247

RESULT 8
US-09-864-761-3473
: Sequence 3473, Application US/09864761

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; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3473
; LENGTH: 1976
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL023280.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HL100, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; US-09-864-761-3473
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Query Match 15.9%; Score 32; DB 3; Length 1976;
Best Local Similarity 65.3%; Pred. No. 4.8;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY 37 CCTGTTTACACCCCGAGACAGCTTCCCTATATCGCTTTCCCTATCAATAGTTTCTAA 96
Db 895 CCTCTTTATCCTTCCAGAGAGCTTCCCTGTATCGGTTAGCCTTTGCATATCCTCTCT 954
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QY 97 CTCATGTGAGTC 108
Db 955 TTCAATTGGGTC 966

RESULT 9
US-10-450-763-8921/c
; Sequence 8921, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 8921
; LENGTH: 2365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (74)..(2362)
; OTHER INFORMATION: 43% homologous to Feline leukemia virus gag-pol precursor
; OTHER INFORMATION: polyprotein gpr80, accession number M18247, Smith-Waterman Score=
; OTHER INFORMATION: 1551.
; US-10-450-763-8921
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Query Match 15.9%; Score 32; DB 9; Length 2365;
Best Local Similarity 65.3%; Pred. No. 5.1;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY 37 CCTGTTTACACCCCGAGACAGCTTCCCTATATCGCTTTCCCTATCAATAGTTTCTAA 96
Db 586 CCTCTTTATCCTTCCAGAGAGCTTCCCTGTATCGGTTAGCCTTTGCATATCCTCTCT 527
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QY 97 CTCATGTGAGTC 108
Db 526 TTCAATTGGGTC 515
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RESULT 10
US-10-450-763-6475/c
; Sequence 6475, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 6475
; LENGTH: 3118
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (66)..(2366)
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LOCATION: (3087) (13008)
 OTHER INFORMATION: 43% homologous to Feline leukemia virus gag-pol precursor
 OTHER INFORMATION: polyprotein gp80, accession number AF052723, Smith-Waterman Score=
 OTHER INFORMATION: 1547
 OTHER INFORMATION:

US-10-450-763-6466

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Query Match      15.9%; Score 32; DB 9; Length 4953;
Best Local Similarity 65.3%; Pred. No. 6.9;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTGCCCTATATCGCTTTCCCTATCAATAGTTTCTAA 96
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Db 820 CCTCTTTAATCCTTCCAGAGAGCTTCCCTGTATCGGTTTAGCCTTTGCATATCCTCTCT 761
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 97 CTCATGTCAGTC 108
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Db 760 TTCATTGGGTC 749
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RESULT 14
US-10-450-763-27114/c
; Sequence 27114, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450, 763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540, 217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649, 167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 27114
; LENGTH: 4953
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (308)..(2608)
; OTHER INFORMATION: 43% homologous to Feline leukemia virus gag-pol precursor
; OTHER INFORMATION: polyprotein gPr80, accession number AF052723, Smith-Waterman Score=
; OTHER INFORMATION: 1547.
US-10-450-763-27114
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Query Match      15.9%; Score 32; DB 9; Length 4953;
Best Local Similarity 65.3%; Pred. No. 6.9;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTGCCCTATATCGCTTTCCCTATCAATAGTTTCTAA 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 820 CCTCTTTAATCCTTCCAGAGAGCTTCCCTGTATCGGTTTAGCCTTTGCATATCCTCTCT 761
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 97 CTCATGTCAGTC 108
    ||| ||| ||| |||
Db 760 TTCATTGGGTC 749
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RESULT 15
US-10-122-851-240/c
; Sequence 240, Application US/10122851
; Publication No. US20050239060A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2BDV3
; CURRENT APPLICATION NUMBER: US/10/122,851
; CURRENT FILING DATE: 2002-04-12
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; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_FL_genes Version 1.0
; SEQ ID NO 240
; LENGTH: 4953
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4953)
US-10-122-851-240

Query Match      15.9%; Score 32; DB 9; Length 4953;
Best Local Similarity 65.3%; Pred. No. 6.9;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTGCCCTATATCGCTTTCCCTATCAATAGTTTCTAA 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 819 CCTCTTTAATCCTTCCAGAGAGCTTCCCTGTATCGGTTTAGCCTTTGCATATCCTCTCT 760
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 97 CTCATGTCAGTC 108
    ||| ||| ||| |||
Db 759 TTCATTGGGTC 748

Search completed: February 16, 2006, 07:57:37
Job time : 174.375 secs
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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 08:16:57 ; Search time 582.92 Seconds
(without alignments)
2854.981 Million cell updates/sec

Title: US-10-041-018-383

Perfect score: 4113

Sequence: 1 MNLSLCTASPLTKSRPAA.....TVKDIYINPLVLVNEEEQR 784

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abbs04
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-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6 -FCGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:

- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	144	3.5	7512	8	US-10-647-956A-7
2	137	3.3	3919	12	Sequence 7, Appli
3	133.5	3.2	8503	12	Sequence 1125, Ap
4	133.5	3.2	8512	12	Sequence 45, Appl
					Sequence 46, Appl

5	131.5	3.2	3444	8	US-10-793-626-4144	Sequence 4144, Ap
6	125	3.0	3735	12	US-11-052-554A-514	Sequence 514, App
7	123.5	3.0	15475	7	US-10-893-483-4	Sequence 4, Appli
8	122.5	3.0	1331	8	US-10-485-517-111	Sequence 111, App
9	121.5	3.0	3729	8	US-10-793-626-3667	Sequence 3667, Ap
10	121.5	3.0	6773	8	US-10-947-249-105	Sequence 105, App
11	121.5	3.0	15071	8	US-10-793-626-2963	Sequence 2963, Ap
12	121	2.9	3146	8	US-10-793-626-3375	Sequence 3375, Ap
13	121	2.9	3569	8	US-10-793-626-4304	Sequence 4304, Ap
14	120.5	2.9	3684	8	US-10-793-626-95	Sequence 95, Appli
15	120.5	2.9	3906	8	US-10-793-626-3870	Sequence 3870, Ap
16	119.5	2.9	2970	8	US-10-793-626-2593	Sequence 2593, Ap
17	119.5	2.9	3549	8	US-10-793-626-3796	Sequence 3796, Ap
18	119.5	2.9	3815	8	US-10-750-185-29584	Sequence 29584, A
19	119.5	2.9	3815	8	US-10-750-623-29584	Sequence 29584, A
20	119.5	2.9	5254	7	US-10-766-317-7	Sequence 7, Appli
21	119.5	2.9	5575	12	US-11-136-527-3245	Sequence 3245, Ap
22	119.5	2.9	14121	12	US-11-124-020A-1	Sequence 10, Appl
23	119.5	2.9	14121	12	US-11-123-656A-3	Sequence 3, Appli
24	118.5	2.9	10170	12	US-11-136-527-1817	Sequence 1817, Ap
25	117	2.8	29942	7	US-10-895-064-3	Sequence 3, Appli
26	117	2.8	29942	7	US-10-895-064-34	Sequence 34, Appl
27	117	2.8	29942	7	US-10-895-064-457	Sequence 457, App
28	117	2.8	29942	7	US-10-895-064-724	Sequence 724, App
29	117	2.8	29942	7	US-10-895-064-1319	Sequence 1319, Ap
30	117	2.8	29942	7	US-10-895-064-1908	Sequence 1908, Ap
31	117	2.8	29942	7	US-10-895-064-2454	Sequence 2454, Ap
32	116.5	2.8	1556	9	US-11-072-512-779	Sequence 779, App
33	116.5	2.8	43445	12	US-11-124-020A-1	Sequence 1, Appli
34	116.5	2.8	43445	12	US-11-124-020A-2	Sequence 2, Appli
35	116	2.8	3866	8	US-10-793-626-3980	Sequence 3980, Ap
36	115.5	2.8	3145	12	US-11-188-743-9	Sequence 9, Appli
37	115.5	2.8	3145	12	US-11-183-294-21	Sequence 21, Appl
38	115.5	2.8	5054	8	US-10-821-234-123	Sequence 123, App
39	115	2.8	4045	8	US-10-793-626-3929	Sequence 3929, Ap
40	115	2.8	4501	12	US-11-136-527-2885	Sequence 2885, Ap
41	114.5	2.8	2292	12	US-11-136-527-2676	Sequence 2676, Ap
42	114.5	2.8	3026	12	US-11-136-527-2868	Sequence 2868, Ap
43	114.5	2.8	3204	8	US-10-793-626-3940	Sequence 3940, Ap
44	114	2.8	3060	8	US-10-793-626-3495	Sequence 3495, Ap
45	114	2.8	10302	12	US-11-127-832-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-10-647-956A-7
; Sequence 7, Application US/10647956A
; Publication No. US20050251878A1
; GENERAL INFORMATION:
; APPLICANT: ffrrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/10/647,956A
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/817,514
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 7512
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
US-10-647-956A-7

Alignment Scores: 0.00197
Pred. No.: 144.00
Length: 7512
Matches: 149

Percent Similarity:	33.0%	Conservative:	118
Best Local Similarity:	18.4%	Mismatches:	257
Query Match:	3.5%	Indels:	284
DB:	8	Gaps:	40
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QY	36	AsnProThrAsnLeuIleleAspThrLysGluArgIleGlnLysGlnPheLysAsn	55
DB	7	AACTATTATCAAGCACTATCGATACTATTGTGAGAAATGCAATTAATCTGTTCGG---	63
QY	56	ValGluIleSerValSerSerTyArgThrAlaThrValAlaMetValProSerProAsn	75
DB	64	CGGGAATTCCTTTGATCCCTTGATCT-----	93
QY	76	SerProLysSerProCysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsn	95
DB	94	-----TTCCGGGAAAAACTCGGGAATGGTTAAT-----	123
QY	96	AspGlySerTrpGlyLeuValAsnHisThrHisAsn-----	107
DB	124	-----TGGGGGGAAGCAAAACGGATTATGAAATTCGCAACGGGAAACAGGATAGA	174
QY	108	-----HisAsnHisProLeuLeuLysAspSerLeu	117
DB	175	AACCTACTTCAGAAAACGTATTTTGGCTATGCTAATCCGCTGCTGAAACCGCTGT	234
QY	118	SerSerThrLeuAlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIle	137
DB	235	-----CGGTTGGGTACCCGGCAAAATG	255
QY	138	AsnLysGlyLeuSerPheIleGlu-----SerAsnLeu-----	148
DB	256	-----TTGGGTTTATACAAGGTTATAGTGATCTGTTGGTAATCGTGTGATAAC	306
QY	149	-----AlaSerAlaThrGluLysSerGlnProSerProIleGlyPheAspIleIlePhe	166
DB	307	TATGCCGCCCGCGGCTCGGTTCGATGTTCTCACCGCGGCTTAT-----TTG	357
QY	167	ProGlyLeuLeuGluTyAlaLysAsnLeu-----AspIleAsnLeuLeuSer	182
DB	358	ACGGAATTCACCGTGAAGCAAAACTTGCATGACAGCAGCTCAATTTATACCTAGAT	417
QY	183	LysGlnThrAsp-----PheSerLeuMetLeuHisLysArgGluLeuGlnLys---	199
DB	418	AAACGTCGCCCGGATTTAGCAAGCTTAATGCTCAGCCAGAAAATATGATGAGGAAAT	477
QY	200	-----ArgCysHisSerAsnGluMetAspGlyTyLeuAlaTyIleSerGluGlyLeu	217
DB	478	TCACCGCTGGCTCTCTTAATGAATG-----TGCCCTTGGCGGGATCGAAACAAACAA	531
QY	218	GlyAsnLeuTyAsp-----TrpAsnMetValLysLysTyGlnMetLysAsnGlySer	235
DB	532	GGAAATCAACAGATGAAGTGATGGATATGTTGCAACTTATCGTTTAAGTGGAGAGACA	591
QY	236	ValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCys	255
DB	592	CCTTATCATCAGCTTATGAAACTGTTCTGTAATCGTTTCATGAACGTGATCCAGGA---	648
QY	256	LeuAsnTyLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyPro	275
DB	649	TTTCGTTCATTTGTCACAG-----GCACCCATTTGT-----	678
QY	276	HisAspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHis	295
DB	679	-----GCTGCTAGCTTCGATCTGCTGACCTTGTGGTGGTATTAGCTCC	720
QY	296	HisPheArgValGluIleLysAsnValLeuAspGluThrTyArgCysTrpValGluArg	315
DB	721	CATATTTCGCCAGAACTGTATAACTTGCTGATTCGATTCGAGGATC-----CCGGAAAAA	771
QY	316	AspGluGlnIle-----PheMetAspValValThrCysAla	327

DB	772	GATGAAGCCGCGCTTGATACGCTTTTATAAAACAACTTTGGCGATATTACTACTGCTCAG	831
QY	328	LeuAlaPheArgLeuLeuArgIleAsnGlyTyArgValSerProAspProLeuAlaGlu	347
DB	832	TTAATGTCCCAAGTTATCTGCCCGGTATTATGCGCTCTCACCGAAGATATTGCTCTAC	891
QY	348	IleThrAsnGluLeuAlaLeuLysAspGluTyAlaAlaLeuGluThrTyHisAlaSer	367
DB	892	GTGACAGCTTCATTA-----	909
QY	368	HisIleLeuTyGlnGluAspLeuSerSerGlyLysGlnIleLeuLysSerAlaAspPhe	387
DB	910	CATGTTGGATATAGCAGTGATATT-----CTGGTTATTCGGTTGGTCGATGCT	957
QY	388	LeuLysGluIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluVal	407
DB	958	GTGGGTAAAGATG-----GAAGTA	975
QY	408	GluAsnAlaLeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgAsn	427
DB	976	GTTCTGTTTACCCGAACACCATCGGATATTATACCATCGTCAGACGAA-----TAT	1026
QY	428	IleGlnLeuTy-----AsnValAspAsnThrArgIleLeuLysThrThrTyHisSer	445
DB	1027	ATTGAGCTGTATCCACAGGTCGCCACATATTATTGATC-----AAA	1068
QY	446	SerAsnIleSerAsnThrAspTyLeuArgLeuAlaValGluAspPheTyThrCysGln	465
DB	1069	TACATCTAAGCAATAGT-----TTTGGTTTGGATGATTTTATCTG-----	1110
QY	466	SerIleTyArgGluGluLeuLysGlyLeuGluArgTrpValValGluAsnLysLeuAsp	485
DB	1110	-----	1110
QY	486	GlnLeuLysPheAlaArgGlnLysThrAlaTyCysTySerPheSerValAlaAlaThrLeu	505
DB	1110	-----	1110
QY	506	SerSerProGluLeuSerAspAlaArgIleSerTrp-----AlaLysAsnGlyIle	522
DB	1111	-----CAATATAAAGATGTTTCGCTGATTCGACTGAGATTGCCCATATCCCTAT	1161
QY	523	LeuThrThrValValAspAspPhePheAspIleGlyGlyThrIle-----AspGluLeu	540
DB	1162	CCTGATATGTCATAAATCAAAAGTATGAATCACAGCGCACAAATCAACGTAGTACTCT	1221
QY	541	ThrAsnLeuIleGlnCys---ValGluLysTrp-----	550
DB	1222	GACATATACTCAGTATAGGTTTACAAGATGCGATAGCGGTAGTTATATTTTGGCGCC	1281
QY	551	---AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAla	569
DB	1282	GCCAAATTTAAAATTTGACCNA-----TACTCCCGGAAAGCTTTCTGCTTAAA	1329
QY	570	LeuLysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspVal	589
DB	1330	ATGAATAAGCTTATCGGTTGCTC-----AAAGTACCAGCCCTC	1368
QY	590	ThrSerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIle	609
DB	1369	TCCTTTGCTACGTTGGAGCGTATTGTTGATAGTGTATATAGC-----	1410
QY	610	TrpThrArgAspAlaTyValProThrLeuAsnGluTyMetGluAsnAlaTyValSer	629
DB	1411	---ACCAATCCATCAGCTTGCAGTTATTAACAAG-----	1443
QY	630	PheAlaLeuGlyProIleValLysProAlaIleTyPheValGlyProLysLeuSerGlu	649
DB	1444	-----GTTATCGGTAATAATTTCTATTATTTGATCGTTATCGCATCAGTAA	1488
QY	650	GluIleValGluSerSerGluTyHisAsnLeuPheLysLeuMetSerThrGlnGlyArg	669
DB	1489	GAGACGCGCTATT-----TTGGCTAATAATATATCTCTCAGCAAGCT	1533

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Qy 670 LeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaVal 689
Db 1534 GTTGGCAATCAGCTTAGCCAGTTGACCAACTATTTAATCACCGCGCTCAATGGTATT 1593
Qy 690 -----AlaLeuHisLeuSerAsnGlyGluSerGlyLysVal 701
Db 1594 CGCTATGAATCAGTAGGACAACTCCAAACATCTTCTTAATCTGTATCTGAACCTTAAA 1653
Qy 702 GluGluValValGluGluMetMetMetMetMetMetMetMetMetMetMetMetMetMet 721
Db 1654 CCAGACAGTACCGGTGATGAT-----CAACGCAAGCGGTTTAA 1692
Qy 722 LysLeuIlePheGluGluAsnGlySerIleValProArgAlaCysLysAspAlaPheTyr 741
Db 1693 AAACGCGGTTTTCAGTTAAGCCAGT----- 1719
Qy 742 AsnMetCysHisValLeuAsnPhePheTyrAlaAsnAspAspGlyPheThrGlyAsnThr 761
Db 1720 GAGTTGATCAGATGTTATTGATCAGTATCGTAAAGACGCGTGTATCAAAAATAAC 1779
Qy 762 IleLeuAspThrValLysAspIle 769
Db 1780 ---TTAGAGAATTGTCTGATCTG 1800
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RESULT 2

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US-11-108-172-1125
; Sequence 1125, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1125
; LENGTH: 3919
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-108-172-1125
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Alignment Scores:
Pred. No.: 0.00437 Length: 3919
Score: 137.00 Matches: 161
Percent Similarity: 35.6% Conservative: 136
Best Local Similarity: 19.3% Mismatches: 300
Query Match: 3.3% Indels: 238
DB: 12 Gaps: 41
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US-10-041-018-383 (1-784) x US-11-108-172-1125 (1-3919)

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Qy 103 AsnHisThrHisAsnHisAsnHisProLeuLeuLeuAspSerLeuSerSerThrLeuAla 122
Db 129 AAGTAC---CAGTCCAAGCAAGAGGAATTACAGAGAGATATGCAAGGAAGTACACAGCA 185
Qy 123 CysIleValAlaLeuLysArgTrpAsnVal-----GlyGluAspGlnIle 137
Db 186 ATGGAAGAATAATAGTCGCAACACAGAACTCTTTTAAAGAGAGCGGTGACGAGTTGTC 245
Qy 138 AsnLysGlyLeuSerPheIleGluSerAsnLeu-----AlaSer 150
Db 246 CAAGCGGATAGAGCTTTGATTGAGCAGAACTGAAACGAGGTGAAGATGAAGTGTGCCAG 305
Qy 151 AlaThrGluLysSerGlnProSerProIleGlyPheAsp----- 163
Db 306 CTGAACCTTAAAGCTGAGCAGTTCGAGAAAGAGTGGATAAGGCAGTGACTACGGCCTC 365
Qy 164 -----IleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAsp 177
Db 366 AAGGAGGAGACTGAAAAGGTTTGACGCTGTGAGGAGCTGGAAGAGACAAACCAAGATA 425
Qy 178 IleAsnLeuLeuSer-----LysGlnThrAspPheSerLeuMetLeu 191
Db 426 GAAATCTTTTGAACCTGGTGTCAATGTGTGAGAGAGACTCCGAGGGGTGTGGACCAAG 485
Qy 192 HisLysArgGluLeuGluLysArgCysHisSerAsnGluMetAspGlyTyrLeuAla 211
Db 486 CACACACACCCATCGAGCAGACGGAACCTATTTCATGAAGTGTATGACAGTTAGGA 545
Qy 212 TyrIleSerGluGly-----LeuGlyAsnLeuTyrAspTrpAsn----- 224
Db 546 GCTGCGCAAGAGAGGATGAAGTCAATGTGTAACCTCTCTGGAGACAGATGCTGAAGGCACAGT 605
Qy 225 -----MetValLysLysTyrGlnMetLysAsnGlySer 235
Db 606 GAGGCCACGAGGGGAATCTGAACACGACAGTATGAGAAAGTCAAGGCCGACGCGGAAG 665
Qy 236 ValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCys 255
Db 666 ATCATGGCTCAGCACCGCGGCTCTTAGCCACGACGAGTCCGCCAG----- 713
Qy 256 LeuAsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrPro 275
Db 714 -----GTGCTGCTTGAGAAACAGGGCCACTATCTGTCC-----CCC 749
Qy 276 HisAsp-----LeuPheIleArgLeuSer 283
Db 750 GAGGAGAAGAGAGAGGCTGCAGAGACACCCAGAGAGCTGAAGGTGCATTTAGGAAGGTG 809
Qy 284 MetValAspThrIleGluArgLeuGlyIleSerHisHisPheArgValGluIleLysAsn 303
Db 810 CTGGCCGAGTGCAGAGAGAGGTGAAGCTCAGCGACTCCCTCCCTGCGAGGAGGAGCTGGAGAG 869
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Qy 368 HisIleLeuTyrGlnGluAspLeuSerSerGlyGlnIleLeuLysSerAlaAspPhe 387
Db 2533 -----ACTGATCAAGAAATTCAAAATTTCAAAACCCCTTCATATGGACTTTGAGCAA 2583
Qy 388 LeuLysGluIleLeuSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluVal 407
Db 2584 AAGTATAAGATGGTCTTCTGAGGAGAAATGAGAGATGAATCAGGAAATAGTTAATCTCTCT 2643
Qy 408 GluAsnAlaLeuLysPheProIleAsnThrGlyLeu----- 419
Db 2644 AAAGAAGCCCAAAATTTGATCGAGTTGGTGCTTTGAAGACCGAGCTTCTTACAAG 2703
Qy 420 -----GluArgIleAsnThrArgArgAsn 427
Db 2704 ACCCAAGAACTTCAGGAGAAAACACGTCGAGTTCAAGAAAGACTTAATATGATGGAACAG 2763
Qy 428 Ile-----GlnLeuTyrAsnValAspAsnThrArgIleLeuLysThrTyrHisSer 445
Db 2764 CTGAAGGAACAATTTAGAAAATAGAGATTTCTACG-----CTGCCAAACTGTAGAAGGGAG 2817
Qy 446 SerAsnIleSerAsnThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGln 465
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Qy 466 SerIleTyrArgGluGluLeuLysGlyLeuGluArgTyrValValGluAsnLysLeuAsp 485
Db 2875 CAA---GAAAAGATGATCTAAACAACACTCAAGAA---AGCTTGCAAAATGAGAGGGAC 2928
Qy 486 GlnLeuLysPheAlaArgGlnLysThrAlaTyrCysTyrPhe-----SerVal 501
Db 2929 CAACCTAAAAGTGTATTCACGATACTGTTAAACATGAATATAGATACTCAAGAACAAATTA 2988
Qy 502 AlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLysAsnGly 521
Db 2989 CGAAATGCTCTTGAGTCTCTGAAACCAACATCAAGAAACAATTAATACACTAAAATCGAAA 3048
Qy 522 IleLeuThrThrValValAspAspPhePhe-----AspIleGlyGlyThrIleAsp 538
Db 3049 ATTCTGAGGAGTTTCCAGGAATTTGCATATGAGGAGAAATACAGGAGAACTTAAGAT 3108
Qy 539 GluLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspLysAspCys 558
Db 3109 GAATTTTCAGCAA-----AAGATGTTGGCATAGATAAAACACAGGATTTG 3153
Qy 559 CysSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGly 578
Db 3154 GAAGCTAAAATACCCAAACACATACTGCAGATGTTAAGGAT----- 3195
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Qy 599 GluLeuMetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyrValProThr 618
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Db 3307 CTAAGGAAATATTTGAAATGACCATTTGAAATC-----CAGGAA 3345
Qy 639 AlaIleTyrPheValGlyProLysLeu-----SerGluGluIleValGluSerSerGlu 656
Db 3346 GAATTAAGACTTCTTGGGGATGAATTTAAAAGCAACAGAGATAGTTGCACAGAAAGAG 3405
Qy 657 TyrHis----- 658
Db 3406 AACCATGCCATAAAGAAAGAGAGAGCTTTCTTAGGACCTGTGCAGACTGGCAGAGTT 3465
Qy 659 -----Asn 659
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Qy 660 LeuPheLysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIleHisSerPheLysArg 679

Db 3526 GTACAAGAAGAGATGAGTGCAGAAAAAGATTAAATGAAATAGAGAATTTTAAAGAAT 3585
Qy 680 GluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSerGly 699
Db 3586 GAATTAAGAACAAGAATTTGACATTTGGAAACATATGGAAAAACAGAGAGCTTTGAGTTGGCT 3645
Qy 700 LysValGluGluGluValValGluMetMetMetMetIleLysAsnLysAsn 717
Db 3646 CAGAACTTAATGAAATTTATGAGGAAGTGAATCTATACCAAGAAAGAAAGTTCTA 3705
Qy 718 LysGluLeuMetLys 722
Db 3706 AAGGAATTCAGAGAAG 3720
RESULT 5
US-10-793-626-4144
; Sequence 4144, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P0348005
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4144
; LENGTH: 3444
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-4144
Alignment Scores:
Pred. No.: 0.0137 Length: 3444
Score: 131.50 Matches: 173
Percent Similarity: 35.0% Conservative: 150
Best Local Similarity: 18.7% Mismatches: 313
Query Match: 3.2% Indels: 290
DB: 8 Gaps: 42
US-10-041-018-383 (1-784) x US-10-793-626-4144 (1-3444)
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Qy 20 AlaLeuSerAlaIleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsn 39
Db 973 GCATTGGAATGATTCATCTATTCT----- 999
Qy 40 LeuIleIleAspThrThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSer 59
Db 1000 TTAATTCATGATGATTTACCAGCAATGGATTAATGACGATTTACCGTAGAGGAAAATTAACA 1059
Qy 60 ValSerSerTyrAspThrAlaTyrValAlaMetValProSerProAsnSerProLysSer 79
Db 1060 AATCATAAAGTTTATGCTGATGGAAGCCATT----- 1092
Qy 80 ProCysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrp 99
Db 1093 -----CTTCTGGTGTGATGCTATTATTAAACAAAAGCTTTT 1125
Qy 100 GlyLeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLysAspSerLeuSerSer 119
Db 1126 GAATTAGTTTCT-----AATGATACCTACCATTTGAAGATAGTGTGAAAGTA 1170
Qy 120 ThrLeuAlaCysIleValAlaLeuLysArgTyrAsnValGlyGlu----- 134

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Db 1171 AGTATTATAAAGACTTTTCAAAGCAAGTGGACATTTGGGAATGCTGGTGGCCAGCG 1230
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Db 1231 CTTGATATGGAAGTGAAGGAAGTCAATTCGTTTAGAACCTTTAGAAATCAATTCATGAA 1290
QY 154 LysSerGlnProSerProIleGlyPheAspIle----- 164
Db 1291 ACTAAGACAGCGCGCTTTACTAAATTTTTCAGTTATGGCTGCGGTAGACATTTGCTCAAAGTA 1350
QY 165 -----IlePheProGlyLeuLeuGluTyrAlaLysAsnLeu----- 176
Db 1351 GAACAAAATATTGCTAAGAAATTTAGATGAATTTAGTCATCATTTTAGGAATGATGTTTCAA 1410
QY 177 -----AspIleAsnLeuLeuSerLysGlnThrAsp 186
Db 1411 ATTAAGATGATTTACTGGATGATGATGGTGAATCAAACTTGGCAAAAAGTAGGC 1470
QY 187 PheSerLeuMetLeuHisLys-----ArgGluLeuGluGln 198
Db 1471 AGTGATATAGTAATCATAAAGTACTTATGTTTCTTACTTTGGAAAAGAGGAGCAGAA 1530
QY 199 LysArgCysHisSerAsnGluMetAspGlyTyrLeuAla----- 211
Db 1531 GAAAAGTTAAACAATCATCAA-----TATCTTGTGATGAACCTGCTTAAATCAAAAT 1581
QY 212 -----TyrIleSerGluGlyLeuGlyAsnLeuTyrAsp-----TyrAsn----- 224
Db 1582 TCTGATCAATATGATACTTCTGNAATTAAGTGATATTGTAGATTATTTCTATACACAGAC 1641
QY 225 -----MetValLysLysTyrGlnMetLysAsnGlySerValPheAsnSerProSerAla 242
Db 1642 CATTAATTTATAAAAAATAT-----ACTATATTAGAATGTCTATTTTA 1686
QY 243 ThrAla-AlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrLeuAsnSerLe 262
Db 1687 ACGTATATAACGCATTTATA-----TCTATAGGTTGTCTTCATAGCTTA---TCTAT 1734
QY 262 uLeuAspLysPheGlyAsnAlaValProThrValTyrProHisAspPheIleArgLe 282
Db 1735 GAGGCAATCTTTT---AAITCT-----TCAATTTATATACAAGAATTTATTCACATTTT 1787
QY 282 uSerMetValAspThrIleGluArgLeuGlyIleSerHisPheArgValGluIleLys 302
Db 1788 ATTTCTA----- 1794
QY 302 sAsnValLeuAspGluThrTyrArgCysTrpVal-----GluArgAspGluGlnIlePh 320
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QY 320 eMetAspValValThrCysAlaLeuAlaPheArgLeuLeuAlaGlyLeuAsnGlyTyrGluVa 340
Db 1842 TACTGATATAGT-----CTCGTTAGATATTTTAACTTTTACAT 1880
QY 340 lSerProAspProLeuAlaGluIleThrAsnGluLeuAlaLeuLysAspGluTyr----- 358
Db 1881 TTTCAAAATAGTGTGTAGTAGTTAGTTCAGAACTCCATGTG-TTAAATCAATGATATAATA 1939
QY 359 -----AlaAlaLeuGluThrTyrHisAlaSerHisIleLeuGlyIleLeu 373
Db 1940 TTCGTAAATTTGAGGTGTTAATTTGCCCCAAAAGTCAAGTGAGACATATATAAATNAGAGA 1999
QY 373 uAspLeuSerSerGlyLysGlnIleLeuLysSerAlaAspPheLeuLysGluIleIleSe 393
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QY 411 uLysPheProIleAsnThrGly----- 418

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QY 435 -AsnThrArgIleLeuLysThrThrTyrHisSerSerAsn-----IleSe 449
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QY 449 rAsnThrAspTyrLeuArg-----LeuAlaValGluAspPheTyrThrCysGln 465
Db 2297 TCAAAATTGATGGGATGAGTACTTGGTACAAATTTCTGCTGTGATGAT-----ACATGCTT 2350
QY 465 nSerIleTyrArgGluGlu-----Le 472
Db 2351 ACTTATTTTCTCGAGACGAAGAAGCGAGTGAAGAAATCAAAACTCGAAATTTTCAATTTATT 2410
QY 472 uLysGlyLeuGluArgTTrpValValGluAsnLysLeuAspGlnLeuLysPheAlaArgGln 492
Db 2411 ATAAGATGCGAATGAAATTTATGTTTACAAACC---TTATCAATAAAACAATTTGCCATTTAT 2467
QY 492 nLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeuSerAs 512
Db 2468 TCACGNACTTGATATAAACTTTTCTCAGCGTCTAACAGTTATGAGTGGTGAAACTGGCTC 2527
QY 512 p-----AlaArgIleSe 516
Db 2528 AGGAAAATCTATCATTTATTGATGCCATTTGGACAGTTAATCGGTATGAGAGCTTCTTCTGA 2587
QY 516 rTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhePheAspIleGlyGlyTh 536
Db 2588 TTACGTCGACATGTTGAAAGAAAGCAATTTATCGAAGGTATCTTTGAT----- 2636
QY 536 rIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAspLys 556
Db 2637 -ATAGACGAGATAAGAGCGCAATTAATATACAGTATCATTAGCTATAGATGTTGATGA 2695
QY 556 sAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeuLys----- 571
Db 2696 AGAT-----TTTTTATTAGTTAAAGAGAAATTTTTCAG 2728
QY 572 -----AspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspVa 589
Db 2729 TTTCTGTAAGATGATTTTGTGCTATTAAATAACAACTGTCACTCTACAG-----GACTT 2782
QY 589 lThrSerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaI 609
Db 2783 AAGAAAA---GTGATGCAAGAACTGCTTCATATTTCATGCTCAACATGAACGCAATCTTT 2839
QY 609 eTrpThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSe 629
Db 2840 ACTTAAGCAAAATATCATCTTCAACTATTAGTATGATTATGACACAAATCAGTATTTCAGA 2899
QY 629 rPheAlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLysLeuSerGln 649
Db 2900 TTTA-----CTTAATCA 2911
QY 649 uGluIleValGluSerSerGluTyrHisAsn-----LeuPheLysLeuMetSe 665
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QY 665 rThrGlnGlyArgLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLys 695
Db 2972 CGGGACCAAGGCTTTTATTACAACGATTAGACTTAATGAAATTTCAATTTAGAGGAA----- 3026
QY 685 sLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSerGlyLysValGluGluGluVa 705
Db 3027 -----CTAACGGAAGCTTCTGAAGAGGCGGAAGTGGACCAACTTGAATCCCATAT 3079
QY 705 l-----ValGluGluMetMetMetIleLysAsnLysArgLysGluLe 720
Db 3080 TAAAGAAATTCAAACCTCCGAAAATAATTAATCTAGCTTTTAAACAATGCATCAAGTTCT 3139

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QY 720 uMetLysLeuIlePheGluAenGlySerIleValProArgAlaCysLysAspAlaPh 740
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Db 3170 GTACGAATTA-----AG 3181
QY 760 nThrIleLeuAspThrValLysAspIleIleTyrAsnProLeuValLeuValAenGluAs 780
Db 3182 CAACTACTTGCACACGATTAAATGATATCGTTCCAGAAAAAATTCGTAGATTTAAAGAGGA 3241
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RESULT 6
US-11-052-554A-514
; Sequence 514, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 514
; LENGTH: 3735
; TYPE: DNA
; ORGANISM: Mycoplasma pneumoniae
US-11-052-554A-514

Alignment Scores:
Pred. No.: 0.072 Length: 3735
Score: 125.00 Matches: 186
Percent Similarity: 34.1% Conservative: 137
Best Local Similarity: 19.6% Mismatches: 338
Query Match: 3.0% Indels: 286
DB: 12 Gaps: 45

US-10-041-018-383 (1-784) x US-11-052-554A-514 (1-3735)

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QY 57 GluIleSerValSerSerTyrAspThrAlaTrpValAlaMetValProSerProAsnSer 76
Db 151 GAA-----CAGGGTAGTTTACAAAGTCCCTAACACGGCTTTAAATAATCCAGTGGCC 204
QY 77 ProLys-----SerProCysPheProGluCysLeuAsnTrpLeuIleAsnAsn 92
Db 205 AACAAACAAATTTATCGCTGCACCACTTTTAAAGACACTAGAACGTTGGTACGAAACAAAC 264
QY 93 GlnLeuAsnAspGlySerTrpGlyLeuValAsnHisThrHisAsnHisAsnHisProLeu 112
Db 265 GAA-----GACAAAAGATTATCCAGTTT 288
QY 113 LeuLysAspSerLeuSerSerThrLeuAlaCysIleValAlaLeuLysArgTrpAsnVal 132
Db 289 TTAAGACACTAAGTCCATGTTGACAGT-----CAGTACACACG 330
QY 133 GlyGluAspGlnIle-----AsnLysGlyLeuSerPheIleGluSerAsn 147
Db 331 GCAGTCGATAAAGTGGTATCAGCATCAGCGCAATAAATCACTT---TTTGTGCAACAAGAT 387

148 Leu-----AlaSerAlaThrGluLysSerGlnPro----- 157
388 TTGTTGGATAACCCCGGTGTAGTGAAGCACTCGGAAAGCGCAAAAGCTGCTTGAACAG 447
158 -----SerProIleGlyPheAspIleIlePheProGlyLeuLeuGluTyrAlaLysAsn 175
448 CTCATTAGTGACTTTGCTAGTCGGGTTTCCAAAAGAACTACCTCAATTACAAAAGAGAT 507
176 LeuAspIleAsnLeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGlu 195
508 GGACAAGTTTCTACTGCTGCATTTACTATGAT-----GAACTACACAAAGAGAA 558
196 LeuGluGlnLys----- 199
559 AGCTGAAAAAACTTTGNAATTTAGTCCCAAGTTTGTAGTGAACAACTAATGATGACTTTTC 618
200 ---ArgCysHisSerAsnGluMetAspGlyTyrLeuAlaTyrIle----- 213
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214 -----SerGluGlyLeuGlyAsnLeuTyrAspTrp 223
679 AGTCAAGTTAACTATAAGTATTCTGCTCCAGTCAAGGGTTAGGTTCAGATCTATAACAGA 738
224 AsnMetValLysLys----- 228
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229 -----TyrGlnMetLysAsnGlySer 235
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290 ---ArgLeuGlyIleSerHisPheArgVal----- 299
1039 GCTAACTTAGTGCAGCTTTAAATTTAAAACTGCAAGTTTTTGAGCAAGATAATGACGAA 1098
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315 ArgAspGluGlnIlePheMetAspValThrCysAlaLeuAlaPheArgLeuLeuArg 334
1153 AAAAGTAAGGACGTAGAAAAAGCTTCCAAAACCTAACGCACTGTTTACATATGATCAAGAA 1212
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1213 GGTAAGCAACAAACAAAGTGCATCAGATCCCAATTTGCTGGCGCTTTAGATGACATTTTGCT 1272
347 -----GluIleThrAsn-----GluLeuAlaLeuLysAspGluTyrAlaAla 360
1273 CAAAACACAAAGCGAGGCTAACTAAAGTAAAGTACGAGCGAGGTAAGAAAGAGAGCT 1332
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381 -----IleLeuLysSerAlaAspPheLeuLysGluIleLeuSerThrAspSer 396
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Qy 100 -----GlyLeuValAsnHisThrHisAsnHis----- 108
Db 1854 TTCACATTGAATGGAATGCTTAATTCACGCAAGAGGACACAGTACGAGATTGG 1913
Qy 109 -----AsnHisProLeuLeuLeuLeuAsp 115
Db 1914 ATTAACAAGAGGATCCAACTATATGCTGCTTCAGGAGACACACCTCATCAGCAAGGAT 1973
Qy 116 SerLeuSerSerThrLeuAlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAsp 135
Db 1974 -----GCATGAGACTGAAGTGAAGGATGAAA----- 2003
Qy 136 GlnIleAsnLysGlyLeuSerPheIleGluSerAsnLeuAlaThrGluLysSer 155
Db 2004 -----AAGATCTCTAAGCTAAT-----GGA 2024
Qy 156 GlnProSerProIleGlyPheAspIlePheProGlyLeuLeuGluTrpAlaLysAsn 175
Db 2025 AATCCAAAAGAGCTGGTGGCCATC----- 2051
Qy 176 LeuAspIleAsnLeuLeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGlu 195
Db 2052 -----CTAATATACAGACAAATAAGACTTTAAACATAAAACTATTAAAGAGAC 2099
Qy 196 LeuGluGlnLysArgCysHisSerAsnGluMetAspGlyTrpLeuAlaTrpIleSerGlu 215
Db 2100 AGAGAA-----GGGCAC-----TATATA----- 2117
Qy 216 GlyLeuGlyAsnLeuTrpAspTrpAsnMetValLys---LysTrpGlnMetLysAsnGly 234
Db 2118 -----ATGATTAAGGATCTATCCACAGAAAGACATT 2150
Qy 235 SerValPheAsn-----SerProSerAlaThrAlaAlaPheIleAsnHisGlnAsn 252
Db 2151 ACTATTATAAATGTATACGCACCT-----AATTACAGGGCG 2186
Qy 253 ProGlyCysLeuAsnTrpLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValPro--- 271
Db 2187 CTGGCC-----TACCTGAAGAAATTAAGGATTTAAGGGAGATATAGACTCA 2237
Qy 272 ---ThrValTrpProHisAspLeuPheIleArgLeuSerMetValAspThrIleGluArg 290
Db 2238 AATAACAATAGTACAGGGGACTTCAACACCCACTCTCACCANTGGACAGATCAACAGA 2297
Qy 291 LeuGlyIleSerHisPheArgValGluIleLysAsnValLeuAsp----- 306
Db 2298 -----CAGAAATTCACACAGGAAACAACTGAGCTAATTGACGCCATAGACCAA 2345
Qy 307 -----GluThrTrpArgCysTrpValGluArgAspGluGlnIlePhe----- 320
Db 2346 ATAGACTAATAGATATCTTCAGAACCTCCACCCACAGACACAGAGTTTCATGTATTC 2405
Qy 320 ----- 320
Db 2406 TCCCCAGTACATGAACTCTCTAGGATTGACCATATATAGGCCATAAAGGGAGCCTT 2465
Qy 321 -----MetAspValValThrCysAlaLeuAlaPheArg-----Leu 332
Db 2466 AACAAAGTTCAAAAAATGAAACTATACCATGCGCTTCTCAGACCATAGTGCAGTGMAA 2525
Qy 333 LeuArgIleAsnGlyTrpGluValSerProAspProLeuAlaGluIle-----ThrAsn 350
Db 2526 CTTGAAATCAACACCAACCAAGATCTCT---ACACCATATGCAAAATATATGGAATGGAC 2582
Qy 351 GluLeuAlaLysAspGluTrpAlaAla----- 360
Db 2583 AACATGATCTTAATGAACAGTGGGTGCATCGAAGAAATTTAAAGAGAAATCAAAAGATT 2642
Qy 361 LeuGluThrTrpHisAlaSerHisIleLeuTrpGlnGluAspLeuSerSerGlyLysGln 380
Db 2643 CTAGAAACAAATGAAATGATACACAACTTATCAAAACCTGTGGGACACAGCAAAAGCA 2702

Qy 381 IleLeuLysSer-----AlaAspPheLeuLysGluIleIleSerThrAsp 395
Db 2703 GTGCTAAGAGAAAGTTTATAGCAATTAGTCCCTACATCAAGAGCTGGAAAGAACCA 2762
Qy 396 SerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAlaLeuLys----- 412
Db 2763 ACAATGAATCTCTCCATGACCTC---AAGGAACTAGAAAAACAGCAGCAANTCAAGCCC 2819
Qy 413 -----PheProIleAsnThrGlyLeuGluArgIleAsnThr 424
Db 2820 AAATCCAAAAGGAGAAAGAAATACTAAAGATCAGAGAAGAAATAAAGCAATTTGAAC 2879
Qy 425 ArgArgAsnIleGlnLeuTrpAsnVal----- 433
Db 2880 AAAAAACAATACAAAAGATCAACAAACCAGGAGCTGGTCTTTGAAAAAATAAACAA 2939
Qy 434 -----AspAsnThrArgIleLeuLys 440
Db 2940 ATTGACACACCAATGGCCCAACTAACCAAAAAAAGAGAGAGAACCCAAATCTGTAA 2999
Qy 441 ThrThrTrpHisSerSerAsnIle---SerAsnThrAspTrpLeuArgLeuAlaValGlu 459
Db 3000 ATCAAGAGATAGTAATGGAAATGTAAACAACCTGACACATAGAAATAAAGAAATCATCAGA 3059
Qy 460 AspPheTrpThrCysGlnSerIleTrpArgGluGluLeuLysGlyLeuGluArgTrpVal 479
Db 3060 AACTACTAC-----AAAGAGATGTATGCTTAACAAATTTGGGAACCTGGAGAA----- 3107
Qy 480 ValGluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThrAlaTrpCysTrpPhe 499
Db 3108 ATGATAGATTCTCTGCACAAA-----TGCCACCTT 3137
Qy 500 SerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLys 519
Db 3138 -----CCTAAACTGCGCGTGAAGATATAGAAATCTAAAC 3173
Qy 520 AsnGlyIleLeuThrValValAspPheAspIleGlyGlyThrIleAspGlu 539
Db 3174 AGACCCATA-----ACATGGAGAA 3194
Qy 540 LeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAspLysAspCys 559
Db 3195 ATTGAATCAGTAATAACGCACATACCGNAAAGAGAGCCCA----- 3236
Qy 560 SerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAsp 579
Db 3237 -----GGACCG 3242
Qy 580 GluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGlnThrTrpLeuGlu 599
Db 3243 GATGGCTTC-----ACTGCCGAATTTTACCGGCATTAGAGAA 3281
Qy 600 LeuMetAsnSerMetLeuArgGluAlaIleTrpThr-----ArgAspAlaTrpValPro 617
Db 3282 CAACTAACCCAGTTCTTCTCAAAATTTCCAAACCGATTGAAAGAGAGGGAATCTCCCA 3341
Qy 618 ThrLeuAsnGluTrpMetGluAsnAlaTrpValSerPheAlaLeuGlyProIleValLys 637
Db 3342 -----AATTCTCTTACGAA----- 3356
Qy 638 ProAlaIleTrpPheValGlyProLysLeuSerGluGluIleValGluSerSerGluTrp 657
Db 3357 ---GCCAATATCACTTAAATTCCTAAGCCCGGAAAAACACACAGCAGAAAGAAACTAC 3413
Qy 658 HisAsnLeuPheLysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIleHisSerPhe 677
Db 3414 AGACCTATC---TCCCTGATGAACATAGATGCAAAATACTCAATAAATCTTGCCA--- 3467
Qy 678 LysArgGluPheLysGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsn----- 695
Db 3468 -----AACCGAATCCAACTACACATCAGAAAGATCAT 3500

RESULT 9
US-10-793-626-3667/c
; Sequence 3667, Application US/10793626
; Publication No. US2005025478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EP

Qy	230	GlnMetIysAsnGlySerValPheAsnSerProSerAlaThrAlaAlaPheIleAsn	249
Db	3067	CAACAAATACGATCGAGTTATT-----GCTGATGCCGAAACAACACTACTTAAAT	3020
Qy	250	His---GlnAsnProGlyCysLeuAsnTyrLeu-----AsnSerLeu	262
Db	3019	CAGACAACAATCCAACTTAGAACCTTTATAAAGTCGATATTGTTAAGGATAATATGTCCTA	2960
Qy	263	LeuAspLys-----PheGly-----AsnAlaVal	270
Db	2959	GCTAACGAAAAATACTATTTGGCGCAGAAAACTCATATGACAAATCAATGCGAAAT	2900
Qy	271	ProThrValTyrProHisAspLeuPheIleArgLeuSerMetValAspThrIleGluArg	290
Db	2899	GATGAAATT--AAACATATGAATTATCTTAATAATGCACAAAAGCAATCTATAAAGAT	2843
Qy	291	LeuGlyIleSerHis--HisPheArgValGluIleLysAsnVal-----	304
Db	2842	ATG---ATTTCCTCAGCAGCATTTAAGAACTGAAGTTAAACAACACTTTCGCAACAAGCTAAA	2786
Qy	305	---LeuAspGluThrTyrArgCysTrrpValGluArgAspGluGlnIlePheMetAspVal	323
Db	2785	ACCTTGATGAAGCTATGAATCACTTGAAGATAAAAACCTCAAGTAGTGATTCAGATACT	2726
Qy	324	Val-----ThrCys	326
Db	2725	ACTTTGCTTAATTACACTGAAGCTTCAGAGGATAAAAAGAAAAAGTAGACCAAACTGTA	2666
Qy	327	AlaLeuAlaPheArgLeuLeu---ArgIleAsnGlyTyrGluValSerProAspProLeu	345
Db	2665	TCATGCTCTCAAGCAATCTATGATAAAATAAATGGCTCAAATGTTAAGTTTAGATCAAGTA	2606
Qy	346	AlaGluIleThrAsnGluLeuAlaLeuLys-----AspGluTyrAla	359
Db	2605	CGACAAGCACTAGAACAACTTAACCTCAAGCATCAGAAAACTCGTGGTGATCAGCGAGTT	2546
Qy	360	AlaLeuGluThrTyrHisAlaSerHisIleLeuTyrGln---GluAspLeuSerSer---	377
Db	2545	GAAGAAGCTAAAGTTTCATGCTAATCAACAATTGACCAATTAAACATCTTAAATTCATTA	2486
Qy	378	-----GlyIysGlnIleLeuLysSerAlaAspPheLeuLysGluIleLeuSer	393
Db	2485	CAACAACAAACTCGGAAAGAAAGTGTTTAAAAACGCAACAAAACTAGAGAATAATCGCTACT	2426
Qy	394	ThrAspSerAsnArgLeu-----	399
Db	2425	GCTAGTAACAATGCTCTGTCATTAACAAGTAATGGGTAAATTAGAACAAATTCATTAAT	2366
Qy	399	-----	399
Db	2365	CATGCTGATCTTATTGAAAATAGTGATTAATTATAGCAAGCCGACGACGACAAAATTATC	2306
Qy	400	-----SerLysLeuIleHisLys	405
Db	2305	GCTTATGATGATGCACTAGAACATGGACAAAGATATACAAAATCTTAAACGCAACCCAAAAT	2246
Qy	406	GluValGluAsnAlaLeuLysPheProIleAsn-----ThrGlyLeuGlu	420
Db	2245	GAAGCAAAAACAACGCGTTTACCAAAATTAATTAATGCAGAAACATCGTTAAATGGTTTCGAA	2186
Qy	421	ArgIleAsn-----	423
Db	2185	AGATTAAATCATGCTAGACCACGAGCTTTAGAAATATATTAATCACTAGAAAAATAAAC	2126
Qy	423	-----	423
Db	2125	AATGCTCAAAAGTCTGCTTTTAGAGGATAAAGTAACGCAATCGCATGATTTATTAGAAATTA	2066
Qy	423	-----	423
Db	2065	GAACATCTTTGTCAACAGAGGGCACAACCTCAATGACATTTATGGGTGAATTAGCTAAACGCA	2006

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QY 424 -----ThrArgAsnIleGlnLeuTyrAsnValAspAsnThr 436
Db 2005 ATGTTAAATAAATACTGCTCAACCAAGCAAGATATAAATATATTAAACCGCATACCTA 1946
QY 437 ArgIleLeuLysThrTyrHisSerSerAsnIle----- 448
Db 1945 CGCAAGATAAATCTTTACTCAAGCTATCAACATGACGTCATGCACTCAACAAAACCTCAA 1886
QY 449 ---SerAsnThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIle 467
Db 1885 GGTCAAGAACTTAGATTTC-----AATGCAATTGATACATTTAAAGATGATATATTCAAA 1832
QY 468 TyrArgGluGluLysGlyLeuGluArgTTPVal-----ValGluAsn 482
Db 1831 ACTAAAGATGCACTTAAACGGTATTGAACGTTTAAACAGCTGCAAAATCAAAAGCAGAAAA 1772
QY 483 LysLeuAsnGlnLeuLysPheAlaArgGlnLysThrAlaTyrCysTyrPheSerValAla 502
Db 1771 CTAATTGATGTTAAATTT----- 1751
QY 503 AlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLysAsnGlyIle 522
Db 1750 -----ATTAATAAAGCTCAATTCACATGCAAAATGATGAAT 1712
QY 523 LeuThrThr-----ValValAspAspPhePheAspIleGly 534
Db 1711 ATGAATACTAATCTTATTGTCACAATTTGCTAGATCGTGAATCAAGCATTTGATTTAAAT 1652
QY 535 GlyThrIle-----AspGluLeuThrAsnLeu-----IleGlnCysVal 547
Db 1651 GATGCAATGAATCTTTAAGAGATGAATTAATATCAAGCTTTCTGTCACAGCAGC 1592
QY 548 GluLysTrpAsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPhe 567
Db 1591 TCAAAATTAT---ATAAATTCAGATGAAGAT----- 1565
QY 568 LeuAlaLeuLysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArg 587
Db 1564 -----TTAAAAACAACAATTTGACCATGCTTTAAGTAATGCTCGAAAAAGTACTTGCAAAA 1511
QY 588 AspValThrSerHisValIleGlnThrTrpLeuLeuMetAsnSerMetLeuArgGlu 607
Db 1510 GAAATGTTAAATAATTAGATGAAATACAAATGAGGGACTCAACAAGTATGAGGAT 1451
QY 608 AlaIleTrpThrArgAspAla----- 614
Db 1450 -----ACTAAAGATGCTTTAAATGGTATCTCAACAGTTTATCAAAAGCTAAAGCTAAA 1400
QY 615 -----TyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAla 631
Db 1399 GCAATTCATACGTACAATCTTTA-----TCTTATATCAATGATGCA 1358
QY 632 LeuGlyProIleValLysProAlaIleTyrPheValGly-----ProLysLeuSerGlu 649
Db 1357 CAGCGTCATATTGCTGAAAGTAAATATTCACAACTCTGATGATTATCATCTTTAGCAAT 1298
QY 650 GluIleValGluSerSerGluTyrHisAsnLeuPheLys-----LeuMet 664
Db 1297 ACATTATCTAAAGCTAGTGAATTAGATAATGCAATGAAAGACTTACGAGATCTCTAGAA 1238
QY 665 SerThrGlnGlyArgLeuLeuAsnAspIleHis-----SerPheLys 678
Db 1237 AGTAATTCAACTTCTGTTCCAAATAGTGTGAATATATTAATGCTGATGAATTTACAA 1178
QY 679 ArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSer 698
Db 1177 ATTGAATTTGATGAGCGGTACACCAAGCAAGTGCACAAAGTCTTAAAACTTCAGAAAT 1118
QY 699 GlyLysValGluGluValVal----- 706
Db 1117 CCAGCAACGATTGCAAGAGTATTAGTCTTAGTCAAGCCATTTACGATACAAAAATGCA 1058
QY 707 -----GluGluMetMetMetMetIleLysAsnLysArgLysGluLeuMetLys 722
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Db 1057 TTGAATGGTGAACAACAGCTCTTGCAACTGAGAAGACGCAAGATTTAAATTAATAAAA 1001
RESULT 10
US-10-947-249-105
; Sequence 105, Application US/10947249
; Publication No. US20050287541A1
; GENERAL INFORMATION:
; APPLICANT: AKIRA NAKAGAWARA
; APPLICANT: MIKI OHIRA
; APPLICANT: SHIN ISHII
; APPLICANT: TAKESHI GOTO
; APPLICANT: HIROYUKI KUBO
; APPLICANT: TAKAHIRO HIRATA
; APPLICANT: YASUKO YOSHIDA
; APPLICANT: SAICHI YAMADA
; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma
; FILE REFERENCE: 117007
; CURRENT APPLICATION NUMBER: US/10/947,249
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/505,614
; PRIOR APPLICATION NUMBER: 2003-09-25
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 6773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-947-249-105
Alignment Scores:
Pred. No.: 0.37 Length: 6773
Score: 121.50 Matches: 117
Percent Similarity: 34.0% Conservative: 100
Best Local Similarity: 18.3% Mismatches: 208
Query Match: 3.0% Indels: 213
DB: 8 Gaps: 28
US-10-041-018-383 (1-784) x US-10-947-249-105 (1-6773)
QY 113 LeuLysAspSerLeuSerSerThrLeuAlaCysIleValAlaLeuLysArgTrpAsnVal 132
Db 416 CTGGAAGAGCAATGATACGCATAGCACTTTTCAGAACAACTTAATTTTCAGAACAA 475
QY 133 GlyGluAspGlnIleAsnLys----- 139
Db 476 TCTGAAGATAATGTTTAAAAAACTACAAGAAGAGATTGAGAAAAATTAGGCCAGCTTTGAG 535
QY 140 ---GlyLeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnProSer 158
Db 536 GAGCAAAATTTTATATCTGCAAAAGCAATTAGACGTCACCACTGATGAAAGAGGAAACA 595
QY 159 ProIleGlyPhe---AspIleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAsp 177
Db 596 GTTACTCAACTCCAAAATATCATTCAGGCTAATTCAGAGTATTCAGCAATACCAAAAATATAT 655
QY 178 IleAsnLeuLeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGlu 197
Db 656 -----AGTTTCAGGAGAGAGCTTTTACAG 679
QY 198 GlnLysArgCysHisSerAsnGluMetAspGlyTyrLeuAlaTyrIleSerGluGlyLeu 217
Db 680 TTGAAAGCTTATACACCAAGAGAGAGTGAAGAGTTGATGTGCCAGATTGCAAGCATCA--- 736
QY 218 GlyAsnLeuTyrAspTrpAsnMetValLysLysTyrGlnMetLysAsnGlySerValPhe 237
Db 737 -----GCTAAGCAACATGAAGCAGAG----- 757
QY 238 AsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsn 257
Db 758 -----ATAAAT 763
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Db      1514 AAGCTCAGAACTGCTTTTACTGAAAAAGATGCCTTCTCGAAACTGTGAATCGCCTCCAG 1573
               |||||  |||  ::::| ||||  ::|  ||:::| |||
Qy      624 GluAsnAlaTyrValSerPheAlaLeuGlyProIleValIleValSerGluTyrHisAsnLeuPheVal 643
               |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1574 GGAGAAATGAAAGTTACTATCTTCAACAGAATTTGGTA----- 1612
Qy      644 GlyProIleValSerGluGluIleValGluSerSerGluTyrHisAsnLeuPheValLeu 663
               |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1613 ---CCAGACTTGAAATACCAATAAAGAACCTTCAAGAAAGAAATCGAGTATACTTACTT 1669
Qy      664 ---MetSerThrGlnGlyArgLeuAsnAspIleHisSerPheIleValGluPheLys 682
               ::::|  ::|  ::::|  |||||  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|
Db      1670 AGTCTCAGTCAAGAGATACCATGTTTAAAGAAATTA----- 1705
Qy      683 GlyGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSerGlyLysValGlu 702
               |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1706 GAAGGAAGAATAATTTCTTCTACT----- 1729
Qy      703 GluGluValValGluGluMetMetMetIleLysAsnLysArgLysGluLeu 720
               |||||  ::::|  ::|  ::::|  ::|  ::::|  ::|  ::::|  ::|  ::::|  ::|
Db      1730 ---GAGGAAAAAGCATGATTTTATAAATAAACTGAAAAATTCCTCCATCAAGAAATG 1780

RESULT 11
US-10-793-626-2963
; Sequence 2963, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2963
; LENGTH: 15071
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-2963

Alignment Scores:
Pred. No.: 1.09 Length: 15071
Score: 121.50 Matches: 174
Percent Similarity: 31.4% Conservative: 133
Best Local Similarity: 17.8% Mismatches: 305
Query Match: 3.0% Indels: 367
DB: 8 Gaps: 44

US-10-041-018-383 (1-784) x US-10-793-626-2963 (1-15071)
Qy      4 SerLeuCysIleAlaSerProLeuLeuThrLysSerAsnArgProAlaAlaLeuSerAla 23
               |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      10099 AGCAGTTTCATATCTCAATCAATATATATCTGTAAACAGACACAGAGTGTCCCAAGCA 10150
Qy      24 IleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleIleAsp 43
               |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      10159 ATTGAAAAAGCAAAATCA-----TTAAAT 10188
Qy      44 ThrThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSerValSerSerTyr 63
               ::::|  ::|  ::::|  |||||  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|
Db      10183 CATGCAATGAAAGCACTTAAACAAATATATAAATAATGTCAGATAAAAGTGTAGATAGT--- 10239
Qy      64 AspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerProCysPhePro 83
               ::::|  ::|  ::::|  ::|  ::::|  ::|  ::::|  ::|  ::::|  ::|
Db      10240 -----AGTCGATTCATTACGAGAGATCAACCTGAAAAAGAGCGGTATCAA 10288
Qy      84 GluCysLeuAsnTrp-----LeuIleAsnAsnGlnLeuAsn---AspGlySerTrp 99

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QY 608 AlaIleTrrPThrArgAspAla----- 614
Db 12265 -----ACTAAGATGCTTAAATGGTATCCAAGTTTATCAAAAGCTAAAGCTAAA 12315
QY 615 -----TyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAla 631
Db 12316 GCAATTCAATACGTACCAATCTTTA-----TCTTATATCAATGATGCA 12357
QY 632 LeuGlyProIleValLysProAlaIleTyrPheValGly-----ProLysLeuSerGlu 649
Db 12358 CAGCGTCATATGCTGAAAGTAATATTCACAACCTCTCATGATTTATCATCTTTAGCAAAAT 12417
QY 650 GluIleValGluSerSerGluTyrHisAsnLeuPheLys-----LeuMet 664
Db 12418 ACATTATCTAAGCTAGTAGTATGATATGATATGCAATGCAATGCAAGACTTACGAGATCTCTAGAA 12477
QY 665 SerThrGlnGlyArgLeuLeuAsnAepIleHis-----SerPheLys 678
Db 12478 AGTAATTCAACTTCTGTCCAAATAGTGTGAATTTATTAATGCTGTGATAAGATTTTACAA 12537
QY 679 ArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSer 698
Db 12538 ATTGAATTTGATGAGCGCTACAAACAGCAAGTGCACAAAGTTCTTAAACTTCAGAAAT 12597
QY 699 GlyLysValGluGluGluValVal----- 706
Db 12598 CCAGCAACGATTGAAGAGTATTAGTCTTAGTCAAGCCATTTACGATACAAAATATGCA 12657
QY 707 -----GluGluMetMetMetMetIleLysAsnLysArgLysGluLeuMetLys 722
Db 12658 TTGAATGGTGAAACCAACGCTCTTGCAACTGAGAGAGCAAGATTTAAATTAATAA 12714

RESULT 12

US-10-793-626-3375/c
; Sequence 3375, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3375
; LENGTH: 3146
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3375

Alignment Scores:
Pred. No.: 0.148 Length: 3146
Score: 121.00 Matches: 126
Percent Similarity: 34.3% Conservative: 105
Best Local Similarity: 18.7% Mismatches: 223
Query Match: 2.9% Indels: 221
DB: 8 Gaps: 27

US-10-041-018-383 (1-784) x US-10-793-626-3375 (1-3146)

QY 174 LysAsnLeuAspIleAsnLeuLeuSerLysGln----- 184
Db 2924 AGACAACTCTCAACTTAACCTAGCTGCGAAAAGAAAGTAAGCGCTCTCTTATATAGTGTG 2865
QY 185 -----ThrAspPheSerLeuMetLeuHisLysArgGluLeuGlu----- 197
Db 2864 AATGACTTAACCGAGTTTAAATGCAACACAAAGTGAAGCGCTAGAGGAATTGGACCAA 2805

QY 198 -----GlnLysArgCysHisSerAsnGluMetAspGlyTyrLeuAla 211
Db 2804 TTAGGTTTTAAATAACCAAGACGTGAACGAGTATCAGATATTGAGGCGGTACTTAAT 2745
QY 212 TyrIleSerGluGlyLeuGlyAsnLeuTyrAspTrpAsnMetValLysLysTyrGlnMet 231
Db 2744 TATATA-----GAGAAATGGCAAGC 2724
QY 232 LysAsnGlySerValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGln 251
Db 2723 AAAAGAGGATCT-----TTATCTTACGAT 2700
QY 252 AsnProGlyCysLeuAsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValPro 271
Db 2699 ATTGATGGTATTGTTTAAAGTTAACGATTATCTCAACAAG-AGAAATGGG----- 2647
QY 272 ThrValTyrProHisAspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeu 291
Db 2646 -----TTATACGCAAAAATCTCC-----AAGATG 2623
QY 292 Gly-IleSerHisPheArgValGluIleLysAsnValLeuAspGluThrTyrArgCy 311
Db 2622 GCGGATTGCTTATAAATTTCCAGCTGAA----- 2595
QY 311 sTrpValGluArgAspGluGlnIlePheMetAspValValThrCysAlaLeuAlaPheAr 331
Db 2594 -----GAAGTTTATACAAAATTTTGGATATTGA 2566
QY 331 gLeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGl 351
Db 2565 GCTAAGTATTGGCGTACGGTCTGTGACACCACTGCAATTTCTAGAACCTGTAAAGT 2506
QY 351 uLeuAlaLeuLysAspGluTyrAlaAlaLeuGluThrTyrHisAlaSerHisLeuLeuTy 371
Db 2505 AGCTGGTACTACAGTTTCAAGAGCCTCACTT-----CATAATGAAGATTTAATACA 2455
QY 371 rGlnGluAspLeuSerSerGlyLysGlnIleLeu-----LysSerAlaAspPheLeuLys 389
Db 2454 TGAAGAGATATACGTATCGAGATAGTGTGTATTAAAAAAGCCGGGACATCATCCC 2395
QY 389 sGluIleIleSerThrAspSerAsnArgLeu-----SerLysLeuIleHisLysGl 406
Db 2394 TGAAGTTGTAAGAAAGTATTTTAGATAGACGACCTAACGATCGGAATTTATCATATGCC 2335
QY 406 uVal-----GluAsnAlaLeuLysPheProIleAsnThrGlyLeuGl 420
Db 2334 AACACATTGCTCTAGTTGTGGACATGAATTAGTTCTGTTTGAAGGAGAGTGTCTTTACG 2275
QY 420 uArgIleAsnThrArgArgAsnIleGlnLeu----- 430
Db 2274 TTGTATTAATCCAAATATGTCAGGCACAGCTTATTGAAGGACTTATACATTTGCTTTCAAG 2215
QY 431 -----TyrAsnValAsp-----AsnThrArgIleLeuLysThrThrTyrHisSerSe 446
Db 2214 ACAAGCGATGAATATAGATGGTTTAGTACTAAATTTATTCATCAGCTATACGNAATCA 2155
QY 446 rAsnIleSerAsn-----ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGl 465
Db 2154 GTTAATCAAGAGATGTCGAGATATTTCTATTGAAAGAGAAGATTTATTACCATTAGA 2095
QY 465 nSerIleTyrArgGluGluLeuLysGlyLeu----- 475
Db 2094 GCGAATGGGAAAGAGAAAGTTTGATAATCTTTTATTAGCGATAGAAAAATCTAAGAACA 2035
QY 475 ----- 475
Db 2034 GTCATTAGACATTTATTATTGCGACTGTGATTAGACATTTAGGTGTAAAGCTAGTCA 1975
QY 476 -----GluArgTrp-----ValValGluAsnLysLe 484
Db 1974 AGTACTTGTCTGACCGATATGAACGATGGATCAACTTTTAAAGTAACCTGAAGTGAATT 1915

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QY 484 uAspGlnLeu-----LysPheAlaArgGlnLysThrAlaTyrCysTyrPh 499
Db | : : : : :
1914 AATTGAATTCAGATATTGGAGATAAATTGCACAACTCTGTGTAAACATATCTCGAAA 1855
QY 499 eSerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLys 519
Db | : : : : :
1854 TAGTGATATTCGTTTCATTATTGAA--AAATTAAGTAATAAAAAATGTTAATATGCTTFA 1798
QY 519 sAsnGlyIleLeuThrValValAlaAspPhePheAspIleGlyGlyThrIleAspG 539
Db | : : : : :
1797 TAAAGGAATTAACAACTGAAATCGAAGTTCATCTGATTTTAGTGGGAAACAAATGTT 1738
QY 539 uLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAlaLysAspCysCy 559
Db | : : : : :
1737 ATTACAGGGAACTCGACCAATGACGAGA----- 1707
QY 559 sSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAs 579
Db | : : : : :
1706 -----AATGAAGCATCTGAATGTTG----- 1686
QY 579 pGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGlnThrTrpLeuGl 599
Db | : : : : :
1685 -----AAAATGCAAGGTGCTAAAGTTACAAGCAGCGTACTTAAAGTACTGATAT 1636
QY 599 uLeuMet-----AsnSerMetLeuArgGluAla----- 608
Db | : : : : :
1635 TGTCAATAGCTGAGCAGATGCGGGTCTAAATTAGCCAAAGCTGAGAAATGTTACTGA 1576
QY 609 -IleTrpThrArgAspAlaTyrValProThr-----LeuAsnGluTyr 622
Db | : : : : :
1575 AATTTGGACTGAAGCAGCATTTATTGAAAAACAAATGGAATCTAATAATTAGAGGATTA 1516
QY 622 rMetGluAsnAlaTyrValSerPheAla-LeuGlyProIleValLysProAlaIleTyrP 642
Db | : : : : :
1515 CGTGAATGAAGCAACAATATTTTACTCATCTCGATACTGTTATTATTAAACGGCTTGG 1456
QY 642 heValGlyProLysLeuSerGluGluIleValGluSerSerGluTyr----- 657
Db | : : : : :
1455 GAGATGGACATAACAACTTCATCAGATAAAGAAACAAAGTGAACATAAGGATACCATA 1396
QY 658 --HisAsnLeuPheLysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIleHisSerP 677
Db | : : : : :
1395 ATAAAATCAAGTGAACAACTAGCCACTGTATAAAAAGTTCAGGTGATACTATAGGA 1336
QY 677 heLysArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeu---HisLeuSerAsnG 696
Db | : : : : :
1335 CTATATTACCTTCAAAGAAAGCCAGCTCGTGGATTATTACAAGATAATATGCGCAATG 1276
QY 696 lYGlusSerGlyLysValGluGluGluValValGluGluMetMetMetIleLysAsnL 716
Db | : : : : :
1275 GTTATAATGGA-----GAAGATTTTGAAGTGGTTTACTA----- 1241
QY 716 ysArgLysGluLeuMetLysLeuIlePheGluGluAsn 728
Db | : : : : :
1240 -----GAATTAGTAAGAAATCTTCCACCAAT 1211

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RESULT 13

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US-10-793-626-4304/c
; Sequence 4304, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4304
; LENGTH: 3569
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4304

Alignment Scores:
Pred. No.: 0.176 Length: 3569
Score: 121.00 Matches: 126
Percent Similarity: 34.3% Conservative: 105
Best Local Similarity: 18.7% Mismatches: 223
Query Match: 2.9% Indels: 221
DB: 8 Gaps: 27

US-10-041-018-383 (1-784) x US-10-793-626-4304 (1-3569)
QY 174 LysAsnLeuAspIleAsnLeuLeuSerLysGln----- 184
Db | : : : : :
2367 AGACAACTTGACTCTAAACTAGCTCGAAAAGAAAGTTAAGCGTCTCTTATATAGTGTG 2308
QY 185 -----ThrAspPheSerLeuMetLeuHisLysArgGluLeuGlu----- 197
Db | : : : : :
2307 AATGACCTTAACCGAGTTTAATGCAACACACAAAGTGAAGCGCTAGAGGAATTGGACCAA 2248
QY 198 -----GlnLysArgCysHisSerAsnGluMetAspGlyTyrLeuAla 211
Db | : : : : :
2247 TTAGGTTTTAAACTAACCAGACGTGAACGAGTATCAGATATTGAGGCGCTACTTAAT 2188
QY 212 TyrIleSerGluGlyLeuGlyAsnLeuTyrAspTrpAsnMetValLysLysTyrGlnMet 231
Db | : : : : :
2187 TATATA-----GAGAAATGGACAAGC 2167
QY 232 LysAsnGlySerValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGln 251
Db | : : : : :
2166 AAAAGAGGATCT-----TTATCTTACGAT 2143
QY 252 AsnProGlyCysLeuAsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValPro 271
Db | : : : : :
2142 ATTGATGGTATTGTTATTAAGTTAAACGATTATCTCAACAAGA-GGAATGGG----- 2090
QY 272 ThrValTyrProHisAspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeu 291
Db | : : : : :
2089 -----TTATACGCAAAATCTCC-----AAGATG 2066
QY 292 Gly-IleSerHisHisPheArgValGluIleLysAsnValLeuAspGluThrTyrArgCy 311
Db | : : : : :
2065 GCGGATTGCTTATAAAATTTCCAGCTCAA----- 2038
QY 311 sTrpValGluArgAspGluGlnIlePheMetAspValValThrCysAlaLeuAlaPheAr 331
Db | : : : : :
2037 -----GAAGTTATTACAAATTTATGATATTGA 2009
QY 331 gLeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGl 351
Db | : : : : :
2008 GCTAAGTATTGGCGTACGGGTGTTGTGACACCAACTGCAATTCAGAACCTGTAAGAGT 1949
QY 351 uLeuAlaLeuLysAspGluTyrAlaAlaLeuGluThrTyrHisAlaSerHisIleLeuTy 371
Db | : : : : :
1948 AGCTGGTACTACAGTTTCAAGAGCCTCACTT-----CATAATGAAGATTTAATACA 1898
QY 371 rGlnGluAspLeuSerSerGlyLysGlnIleLeu-----LysSerAlaAspPheLeu 389
Db | : : : : :
1897 TGAAGAGATATACGTATCGGAGATAGTGTGTTATTAAAAAGCGCGGACATCATCCC 1838
QY 389 sGluIleIleSerThrAspSerAsnArgLeu-----SerLysLeuIleHisLysGl 406
Db | : : : : :
1837 TGAAGTTGTAAAAAGTATTTTAGATAGACGACCTAACGAATCGAAATTTATCATATGCC 1778
QY 406 uVal-----GluAsnAlaLeuLysPheProIleAsnThrGlyLeuGl 420
Db | : : : : :
1777 AACACATTGCTCCTAGTTGTGGACATGAATTAGTTGTTTGAAGGAGAGAGTTGCTTTACG 1718
QY 420 uArgIleAsnThrArgArgAsnIleGlnLeu----- 430

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Db 1717 TTTGTAATTAATCCAAATGTCAGGCACAGCTTATTGAAGGACTTATACATTTTCGTTTCAAG 1658
Qy 431 -----TyrAsnValasp-----AsnThrArgIleLeuLysThrThyHisSerSe 446
Db 1657 ACAAGCGATGAATATAGATGGTTTGAAGTACTTAAATTTATTCATCAGCTATACGAAATCA 1598
Qy 446 xAsnIleSerAsn---ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysG1 465
Db 1597 GTTAATCAAGATGTCGAGATTTTCTATTGAAAGAGAGATTTATTACCATAGA 1538
Qy 465 nSerIleTyrArgGluGluLysGlyLeu----- 475
Db 1537 GCGAATGGGAAGAGAAAGCTGTATACTCTTTATTAGCATAGAAAAATCTAAAGACA 1478
Qy 475 ----- 475
Db 1477 GTCATTAGAGCATTTATTATTGCGACTTGTGTATTAGACATTTAGGTGTTAAAGCTAGTCA 1418
Qy 476 -----GluArgTrrp-----ValValGluAsnLysLe 484
Db 1417 AGTACTTGTGAGCGATATGAACGATGGATCAACTTTTAAAGTAACCTGAAGTGAAT 1358
Qy 484 uAspGlnLeu-----LysPheAlaArgGlnLysThrAlaTyrCysTyrPh 499
Db 1357 AATTGAATTCAGATATTGGAGATAAACTTGCACAATCTGTTGTAACATATCTCGAAAA 1298
Qy 499 eSerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaly 519
Db 1297 TAGTGATATTTCGTTCAATTAATGAA---AAATTAAGTAATAAAAAATGTTAATATGCTTA 1241
Qy 519 sAsnGlyIleLeuThrValValAspAspPheAspIleGlyGlyThrIleAspG1 539
Db 1240 TAAGGAATTAACAACTGAAATCGAGTCTCTGATTTTAGTGGGAAACAATGTT 1181
Qy 539 uLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAspLysAspCysCy 559
Db 1180 ATTAACAGGGAACCTCGAGCAAAATGACGAGA----- 1150
Qy 559 sSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAs 579
Db 1149 -----AATGAAGCATCTCAATGGTTG----- 1129
Qy 579 pGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGlnThrTrpLeuG1 599
Db 1128 -----AAATCGAAGTCTAAAGTTACAGCAGCGTGAATAAAGTACTGATAT 1079
Qy 599 uLeuMet-----AsnSerMetLeuArgGluAla----- 608
Db 1078 TGTCTAGCTGGAGCAGATCGGGTCTAAATTTAGCCAAAGCTGAGAGATATGTACTGA 1019
Qy 609 -IleTrpThrArgAspAlaTyrValProThr-----LeuAsnGluTyr 622
Db 1018 AATTTGCACTGAAGCAGCATTTATTGAAAAACAAATGGAATCTAATAATTTAGAGGAGTA 959
Qy 622 rMetGluAsnAlaTyrValSerPheAla-LeuGlyProIleValLysProAlaIleTyrP 642
Db 958 CGTGAATGAAGCGCAACAATATTTTTACTATGTCGATCTGTTATTATTAAACGGCTGGC 899
Qy 642 heValGlyProLysLeuSerGluGluIleValGluSerSerGluTyr----- 657
Db 898 GAGATGCACATAACAACTTCATCATAGATAAAGAACAAAGTGAACATAGGATAACCATTA 839
Qy 658 --HisAsnLeuPheLysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIleHisSerP 677
Db 838 ATAAAAAATCAAGTGAACAAATAGACCACTGATAAAAAAGTTCAAGGTGATTAACATAGGA 779
Qy 677 heLysArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeu---HisLeuSerAsnG 696
Db 778 CTATATTACCTTCAAGAAAGCGCAGCTGCTGGATTATTACAAGATAATATGCGCAATG 719
Qy 696 lYgluSerGlyLysValGluGluGluValValGluGluMetMetMetMetMetMetMetMet 716
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Db 718 GTTATAATGGA-----GAAGATTTTGAAGTGGTTTACTA----- 684
Qy 716 ySArgLysGluLeuMetLysLeuIlePheGluGluAsn 728
Db 683 -----GAATTAAGTAAGAAATCTTCTCCAAACAAT 654

RESULT 14
US-10-793-626-95
; Sequence 95, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-95

Alignment Scores:
Pred. No.: 0.207 Length: 3684
Score: 120.50 Matches: 125
Percent Similarity: 36.0% Conservative: 93
Best Local Similarity: 20.7% Mismatches: 258
Query Match: 2.9% Indels: 129
DB: 8 Gaps: 30

US-10-041-018-383 (1-784) x US-10-793-626-95 (1-3684)

Qy 42 IleAspThrThyLysGluArgIleGlnLysGlnPheLysAsn-----ValGluIle 58
Db 1834 GTAGATAAATAATAATCAACATTTAGCTGAAATAATTAAGCATCAACATCCAGCTGATTAC 1893
Qy 59 SerValSerSerTyrAspThrAlaTrpValAlaMetValProSerProAsnSerProLys 78
Db 1894 AATGTHACAGCTGCTCGTATGGCTGCTTGCCTTCATATCCACAGTTAATAAA---AAC 1950
Qy 79 SerProCysPheProGlu-----CysLeu 86
Db 1951 AGTCTATTATTGTCGAGAGGCTAAAGATGAAGGTGATGATTCAAATGAAGCATCTTA 2010
Qy 87 AsnTrpLeuIleAsnAsnGlnLeuAsn---AspGlySerTrpGlyLeuValAsnHisThr 105
Db 2011 CAAAAAGCGATTCGAATCAGTTAAATAAAGATACACAATTTGCGATAGAAGATCCAGAT 2070
Qy 106 HisAsnHisAsnHisPro-----LeuLeuLysAspSerLeuSerSerThrLeu 121
Db 2071 TTAAGAAAAAACCACTTAATAAACATTTATTGAGAGATCTAATTTAATTTCTAGTTCA 2130
Qy 122 AlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeu 141
Db 2131 GCT-----AAAGGACAAAGATATCTTTATGAAGACACTTG 2163
Qy 142 SerPheIleGluSerAsnLeu---AlaSerAlaThrGluLysSerGlnProSerProIle 160
Db 2164 TTAGGTGCGCTCTGCTGTTTAAATGCGCAGAGCCAAATGAAGATGATAAACAGAGGAAT 2223
Qy 161 GlyPheAspIleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsnLeu 180
Db 2224 AAATGGCGGAGGATACAGAGGAAACTTGATTATTAGTATCACTTGTATTTCAGAAATG 2283
Qy 181 LeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGluGlnLysArg 200
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Db 2284 ACTGCAGCCATTATATTCAGATATCGTTTACCTGCTGCAACTTGGTATGAAACAT 2343
Qy 201 ---CysHisSerAsnGluMetAspGlyTyrLeuAlaTyrIleSerGluGlyLeuGlyAsn 219
Db 2344 GATTTATCTTACAGACATGATCCATTTATTCATCCATTTAAACCCAGGATTCACCA 2403
Qy 220 LeuTyr-----AspTrpAsnMetValLysLysTyrGlnMetLysAsnGlySer 235
Db 2404 TTATGGGAATCCGTTCCGAGCTGGGATATTTATAA-----ACT 2442
Qy 236 ValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCys 255
Db 2443 CTAAGTAAAGCTGTTTCAGAAATGGCGAAGATTATCTT-----CCAGGT--- 2487
Qy 256 LeuAsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrPro 275
Db 2488 -----AAATTTAAAGATGTCGTAACTACACCATTAGGA 2520
Qy 276 HisAspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHis 295
Db 2521 CATGAT-----TCAAAACAAGAAATTTCAACTGAATACGCTATTGTAA 2565
Qy 296 HisPhe---ArgValGluIleLysAsnValLeuAspGluThrTyrArgCysTrp----- 312
Db 2566 GATTGGCTTAAAGGAGAAATGAGGTGGCCAGGTAAACCAATGCCTAATTTTCTATC 2625
Qy 313 ValGluArgAsp---GluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg 331
Db 2626 GTAGAGCGAGACTATACACAAATTTACGATAAATTCGTTTACTGTTGGTCCAAAACCTAGAA 2685
Qy 332 LeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu 351
Db 2685 AAAGGGAATAAGTGTCTCATGTGTGAGT----- 2715
Qy 352 LeuAlaLeuLysAspGluTyrAlaAlaLeuGlu-----ThrTyrHisAlaSer 367
Db 2716 TATAGGTTAGTGAGAGACGACGAGAACTTAAAGTATAGTTAGTGGAACTTGGAAATGATGAT 2775
Qy 368 His---IleLeuTyrGlnGluAspLeuSerSerGlyLysGlnIleLeuLysSerAlaAsp 386
Db 2776 AATACTATTTCAGTTAAATAATGATAGCCGAGAAATAGATACACGCGAGAAAAGTAGCAGAT 2835
Qy 387 PheLeuLysGluIleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGlu 406
Db 2836 GTCATTTTGAATATATCTCTGCTCAAAACGGCAATTTATCAAAAGTCATATGAAGAT 2895
Qy 407 ValGluAsnAlaLeuLysPheProIleAsnThrGlyLeuGlu-----Arg 421
Db 2896 TTAGAAAAT-----CAACAGGTATGGAACCTTAAGATATTTCTAAA 2937
Qy 422 IleAsnThrArgAsnIleGlnLeuTyrAsnValAspAsn-----ThrArgIleLeu 439
Db 2938 GAACGTGCTTCGAAAAGATATCATCTTTAAACATTACTTCTCAACCAAGAGAGTGAT 2997
Qy 440 LysThrTyrThrHisSerSerAsnIleSerAsnThrAspTyrLeuArgLeuAlaValGlu 459
Db 2998 CCAACTGCAGTATTCCTCGC-----TCTAATAAGATGGAAGCGCTACTCACCGTTT 3051
Qy 460 AspPheTyrThrCysGlnSerIleTyrArgGluGluLeuLysGlyLeuGluArgTrpVal 479
Db 3052 ACACTAATGTTGAGCGTTTAGTGCCATTTAGAACACTATAGACACTAATCTGGACGTCAGAGTTATTAT 3111
Qy 480 ValGluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThrAlaTyrCysTyrPhe 499
Db 3112 ATAGATCATGAGGTATTCCAA---CAGTTTGGCGAAAGTTTACCGGTATAT----- 3159
Qy 500 SerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLys 519
Db 3160 -----AAACCTACTTTA---CCTCCAATGGTATTTTGGTCTCGTATAAAAAGTTAAA 3210
Qy 520 AsnGlyIleLeuThrThrValValAspAspPheAspIleGlyGlyThrIleAspGlu 539
Db 3211 GGTGGACAGATACATTAGTGCTTCGATACCTTACCTCATGGG----- 3255

Qy 540 LeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAspLysAspCysCys 559
Db 3256 -----AAATGGAATATT-----CATTCAACTTAT 3279
Qy 560 SerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAsp 579
Db 3280 CAAGATAATGAACGATGTTGACGTTGTTAGAGGTGGACCACTGTATGGATTTCAAT 3339
Qy 580 GluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIle-----GlnThrTrp 597
Db 3340 GAA-----GACGCGCTGACCATGTTATTAATGATAACGACTGG 3378
Qy 598 LeuGluLeuMetAsn 602
Db 3379 TTAGAAGTATACAAC 3393
RESULT 15
US-10-793-626-3870/c
; Sequence 3870, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3870
; LENGTH: 3906
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3870
Alignment Scores:
Pred. No.: 0.224 Length: 3906
Score: 120.50 Matches: 125
Percent Similarity: 36.0% Conservatives: 93
Best Local Similarity: 20.7% Mismatches: 258
Query Match: 2.9% Indels: 129
DB: 8 Gaps: 30
US-10-041-018-383 (1-784) x US-10-793-626-3870 (1-3906)
Qy 42 IleAspThrThrLysGluArgIleGlnLysGlnPheLysAsn-----ValGluIle 58
Db 2120 GTAGATAAATTAATTAATCACCATTAGCTGAAATAATTAAGCATCAACATCCAGCTGATTAC 2061
Qy 59 SerValSerSerTyrAspThrAlaTrpValAlaMetValProSerProAsnSerProLys 78
Db 2060 AATGTAACAGCTGCTCGTATGGCTGGTTCCTTCATATCCACAGTTTAATAA---AAC 2004
Qy 79 SerProCysPheProGlu-----CysLeu 86
Db 2003 AGTCTATTATTGGTGGAGAGGCTAAAGATGAAGGTGATGATTCAAATGAAGCCATCTTA 1944
Qy 87 AsnTrpLeuIleAsnAsnGlnLeuAsn---AspGlySerTrpGlyLeuValAsnHisThr 105
Db 1943 CAAAAAGCGATTGAATCAGTCTAAATAAAGATACACAATTTCCGATAGAAGATCCAGAT 1884
Qy 106 HisAsnHisAsnHisPro-----LeuLeuLysAspSerLeuSerSerThrLeu 121
Db 1883 TTAAGAAAAAACCTCTCTAAACATTTTGTATGGAGATCTAAATTTTCTAGTTCA 1824
Qy 122 AlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeu 141
Db 1823 GCT-----AAAGGACAAGATACCTTTTATGAAGCACTTG 1791

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QY 142 SerPheIleGluSerAsnLeu---AlaSerAlaThrGluLysSerGlnProSerProIle 160
Db 1790 TTAGTGGCGGCTCTGGTTAATGGCAGAGCCAAATGAAGATGATAAACAGAGGAAAT 1731
QY 161 GlyPheAspIlePheProGlyLeuLeuGluTyraAlaLysAsnLeuAspIleAsnLeu 180
Db 1730 AAATGGCGGAGGATACAGAAAGGAAACTTGATTTATTAGTATCACTTGATTTCAAGATG 1671
QY 181 LeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGlnLysArg 200
Db 1670 ACTGGACGCCATATATTACAGATATCGTTTACCTGCTGCTGCACTTGGTATGAAACAT 1611
QY 201 ---CysHisSerAsnGluMetAspGlyTyraLeuAlaTyraIleSerGluGlyLeuGlyAsn 219
Db 1610 GATTATCTCTACAGACATGCATCCATTTATTCATCCATTAACCCAGGATGACCCA 1551
QY 220 LeuTyr-----AspTrpAsnMetValLysLysTyraGlnMetLysAsnGlySer 235
Db 1550 TTATGGGAATCGCGTTCCGACTGGGATATTTATAAA-----ACT 1512
QY 236 ValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCys 255
Db 1511 CTAAGTAAAGCTGTTTCAGAAATGGCGAAAGATTATCTT-----CCAGGT--- 1467
QY 256 LeuAsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrPro 275
Db 1466 -----AAATTTAAGATGTCGTAACTACACCATTAGGA 1434
QY 276 HisAspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHis 295
Db 1433 CATGAT-----TCAAAACAAGAAATTTCAACTGAATACGTTATGTAAAA 1389
QY 296 HisPhe---ArgValGluIleLysAsnValLeuAspGluThrTyrArgCysTrp----- 312
Db 1388 GATTGGTCTAAAGGAGAAATTCGAAGGTGCCAGGTAAACAATGCTTAATTTTCTATC 1329
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QY 332 LeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu 351
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QY 580 GluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIle-----GlnThrTrp 597
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Job time : 653.92 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 07:57:49 ; Search time 1700.42 Seconds
(without alignments)
3812.705 Million cell updates/sec

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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-MAXLEN=2000000000 -HOST=abs04
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6 -FCAPEXT=7
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Database : Published Applications NA.Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4026	97.9	3117	7	US-10-041-018-362
3	2855.5	69.4	2594	7	US-10-041-018-368
4	2107.5	51.2	2638	7	US-10-041-018-367
5	2023.5	49.2	2658	7	US-10-041-018-378
6	2023.5	49.2	2658	7	US-10-041-018-381
7	2022.5	49.2	2506	7	US-10-041-018-377

8	1677	40.8	2554	7	US-10-425-114-3441	Sequence 3441, Ap
9	1668	40.6	2716	8	US-10-425-115-22041	Sequence 22041, A
10	1611	39.2	2730	8	US-10-425-115-22042	Sequence 22042, A
11	1607	39.1	80374	7	US-10-041-018-376	Sequence 376, App
12	1537.5	37.4	2223	6	US-10-259-194A-107	Sequence 107, App
13	1442.5	35.1	2070	7	US-10-437-963-19081	Sequence 19081, A
14	1337	32.5	2029	7	US-10-425-114-5988	Sequence 5988, Ap
15	1319	32.1	2313	7	US-10-437-963-36043	Sequence 36043, A
16	1273	31.0	2193	7	US-10-437-963-72156	Sequence 72156, A
17	1254	30.5	2086	7	US-10-425-114-17004	Sequence 17004, A
18	1247	30.3	2364	8	US-10-425-115-175619	Sequence 175619, A
19	1209	29.4	3666	7	US-10-437-963-72152	Sequence 72152, A
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21	1084.5	26.4	2705	5	US-10-041-007-1	Sequence 1, Appli
22	1084.5	26.4	2705	5	US-10-041-018-397	Sequence 397, App
23	1075	26.1	2388	5	US-10-041-007-36	Sequence 36, Appl
24	1075	26.1	2445	5	US-10-041-007-34	Sequence 34, Appl
25	1075	26.1	2622	5	US-10-041-007-32	Sequence 32, Appl
26	1062.5	25.8	2861	3	US-09-895-752-55	Sequence 55, Appl
27	1062.5	25.8	2861	3	US-09-887-586A-55	Sequence 55, Appl
28	1062.5	25.8	2861	3	US-09-903-012-55	Sequence 55, Appl
29	1062.5	25.8	2861	3	US-09-900-797-55	Sequence 55, Appl
30	1062.5	25.8	2861	3	US-09-893-820-55	Sequence 55, Appl
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32	1062.5	25.8	2861	7	US-10-041-018-365	Sequence 365, App
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ALIGNMENTS

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; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; PRIOR FILING DATE: 2002-01-07
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 361
; LENGTH: 2792
; TYPE: DNA
; ORGANISM: Stevia rebaudiana
US-10-041-018-361

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Percent Similarity: 100.0%
Best Local Similarity: 100.0%
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Conservative: 0
Mismatches: 0
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Gaps: 0
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; Sequence 362, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Mateuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041.018
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 362
; LENGTH: 3117
; TYPE: DNA
; ORGANISM: Stevia rebaudiana
US-10-041-018-362
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Query Match: 79.9% Indels: 0
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Qy 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLysAspSerLeuSerSerThr 120
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Qy 301 IleLysAsnValLeuAspGluThrTyraArgCysTrpValGluArgAspGluGlnIlePhe 320
Db 1400 ATTAATAATGTTTTAGATGAACATACAGATGTTGGGTGGAAACGAGATGAGCAATATTC 1459
Qy 321 MetAspValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsnGlyTyraGluVal 340
Db 1460 ATGGATGTTGTAACATGTGCTTTAGCCTTTTCGGTTATTAAAGGATCCACGGGTATAAAGTC 1519
Qy 341 SerProAspProLeuAlaGluIleThrAsnGluLeuAlaLeuLysAspGluTyraAlaAla 360
Db 1520 TCCCCAGATCAATTTGGCTGAAATTTACTAATGAATTAGCTTTTCAAAAGACGAATACGCAGCT 1579
Qy 361 LeuGluThrTyraHisAlaSerHisIleLeuTyraGlnGluAspLeuSerSerGlyLysGln 380
Db 1580 CTTGAACATATCATGCATCACAGATATATATACAAAGAGATTTATCTTCTCGAAAAACAA 1639
Qy 381 IleLeuLysSerAlaAspPheLeuLysGluIleIleSerThrAspSerAsnArgLeuSer 400
Db 1640 ATCTTGAAGTCAGCTGATTTCTTCAAAAGGATATTTATCCACTGATTCAAACAGGCTTTCT 1699
Qy 401 LysLeuIleHisLysGluValGluAsnAlaLeuLysPheProIleAsnThrGlyLeuGlu 420
Db 1700 AAATTAATTCACAAAGAGTGGAAAAATGCTCTTAAGTTCCTATCAATACCGGTTTAGAA 1759
Qy 421 ArgIleAsnThrArgAsnIleGlnLeuTyraAsnValAspAsnThrArgIleLeuLys 440
Db 1760 CGCTAAACACTAGAGCAAAATATACAGCTTTTACAATGTAGACAAATCAAGAATTTCTGAAA 1819
Qy 441 ThrThrTyraHisSerSerAsnIleSerAsnThrAspTyraLeuArgLeuAlaValGluAsp 460
Db 1820 ACTACATATCACTCATCAATATATAGTACACTTATTTACCTTAGGTGGCTGTGTAAGAT 1879
Qy 461 PheTyraCysGlnSerIleTyraArgGluGluLeuLysGlyLeuGluArgTrpValVal 480
Db 1880 TTCTACACCTGCCAAATCTATTTATCGTGAAGAAATTAAGGCTCTTGAAGGTGGTGGTA 1939
Qy 481 GluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThrAlaTyraCysTyraPheSer 500
Db 1940 CAGAAATAAGTTGGACACAGCTCAAGTTTGGTAGCAAAAGACCCGCTACTGTTATTTCTCT 1999
Qy 501 ValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLysAsn 520

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Db      2000 GTTGTGCAACACTTTCGTCCTCCGAATATTACAGATCGCGTATTTCATGGGCCAAAAT 2059
Qy      521 GlyLeuThrValValAspPheAaspPheAaspGlyThrIleAspGluLeu 540
Db      2060 GGCATATTAACTACAGTAGTTCATGCTTTTGGATATCGGTGATCAATCGATGAATG 2119
Qy      541 ThrAsnLeuIleGlnCysValGluIleThrAsnValAspValAspCysSer 560
Db      2120 ACCAACTGATTCATGCTTGAATAATGGAATGTAGATGTGCACAAGGATTTGTTGTCA 2179
Qy      561 GluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAspGlu 580
Db      2180 GAGCATGTTCCGATTTATTTTATAGCATTAAGATGCAATCTGTTGGATGGAGATGAA 2239
Qy      581 AlaPheLeuTrpGlnAlaArgAspValThrSerHisValIleGlnThrTrpLeuGluLeu 600
Db      2240 GCTTTTAAATGCAAGCGCGCATGTAACTAGCATGTTTATTCAAACTTTGGTTGGAACCTA 2299
Qy      601 MetAsnSerMetLeuArgGluAlaIleThrTrpThrArgAspAlaIleValProThrLeuAsn 620
Db      2300 ATGAATAGTATGTGTGAGAAGCTATATGCAAGAGATGCTTATGTGCCAACATTAAT 2359
Qy      621 GluTrpMetGluAsnAlaIleValSerPheAlaLeuGlyProIleValLysProAlaIle 640
Db      2360 GAATATATGGAACACCTTACGTGTTCATTTAGCATAGCCCGCATTTGCAAGCCGCTATT 2419
Qy      641 TyrPheValGlyProLysLeuSerGluGluIleValGluSerSerGluTrpHisAsnLeu 660
Db      2420 TACTTTGTGGGCCCAAAATATATCAGAGGAGATTGTTGAAAGCTCTGAAATATCATAATCTA 2479
Qy      661 PheLysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIleHisSerPheLysArgGlu 680
Db      2480 TTTAAGCTAATGAGCAGCGAGGTTCGACTTCTTAAACGATATCCATAGCTTCAAGAGGGAA 2539
Qy      681 PheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSerGlyLys 700
Db      2540 TTTAAGAAAGGCMAATTAACCGGTAGCATTTGCATTTGATGTAACGGAGAAAGTGGAAA 2599
Qy      701 ValGluGluGluValValGluMetMetMetMetMetMetMetMetMetMetMetMetMet 720
Db      2600 GTGGAAGAGAGAGGTTGTGGAGGAGATGATGATGATGATGATGATGATGATGATGATGAT 2659
Qy      721 MetLysLeuIlePheGluGluAsnGlySerIleValProArgAlaCysLysAspAlaPhe 740
Db      2660 ATGAAATTAATTTTGAAGAAAATGCTAGCATTTGCTTAGAGCTTGTAAAGATGCAATTT 2719
Qy      741 TrpAsnMetCysHisValLeuAsnPhePheTrpAlaAsnAspAspGlyPheThrGlyAsn 760
Db      2720 TGGAACTGTGTCAGCTGTGTGAATTTTATTTTACGCAACGATGACGGGTTTACTGGAAAC 2779
Qy      761 ThrIleLeuAspThrValLysAspIleIleTrpAsnProLeuValLeuValAsnGluLeu 780
Db      2780 ACGATTCTTGATACGTGGAAGGACATCAATTTACAACCCGTTGGTCTGTGATGAATGAAT 2839
Qy      781 GluGluGlnArg 784
Db      2840 GAAGAACAAGG 2851

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RESULT 3

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US-10-041-018-368
; Sequence 368, Application US/10041018
; Publication No. US2004007232A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080051/10025547
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 368
; LENGTH: 2594
; TYPE: DNA
; ORGANISM: Lactuca sativa
US-10-041-018-368

Alignment Scores:
Pred. No.: 1,7e-269 Length: 2594
Score: 2855.50 Matches: 541
Percent Similarity: 80.6% Conservative: 102
Best Local Similarity: 67.8% Mismatches: 116
Query Match: 69.4% Indels: 39
DB: 7 Gaps: 6

US-10-041-018-383 (1-784) x US-10-041-018-368 (1-2594)
Qy      1 MetAsnLeuSerLeuCysIleAlaSerProLeuLeuThrLysSerAsn----- 16
Db      87 ATGAATATCGCACAGATCATCATCCGCCATCGCTGCTTCTCGTCACACATACCACAT 146
Qy      17 -----ArgProAlaAlaLeuSerAlaIle 24
Db      147 CGCTCATGGGTGTTAAATTGCTGTATGGTGCATAACAACCCA-----TCGGGTCTT 197
Qy      25 HisThrAlaSerThrSerHisGlyGlnThrAsnProThrAsnLeuIleIleAspThr 44
Db      198 CGTACAGCTTCT-TCACAAGCTGCACAAGTTAATCTCTACTGTCTATGACCTTGTATGTG 254
Qy      45 ThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSerValSerTrpAsp 64
Db      255 ACCAAGAAAGCAATCGGAAGCTGTTCAACATGTGGAAAGTTCTGTTTCTTCATATGAC 314
Qy      65 ThrAlaTrpValAlaMetValProSerProAsnSerProLysSerProCysPheProGlu 84
Db      315 ACAGCTTGGTAGCCATGCTCCTCCAAACTCTCCAAATCCCTTGTGTTTCCCTGAT 374
Qy      85 CysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHis 104
Db      375 TGTCTGAAGTGGTTACTGGATAATCAGCTTGATGATGGTTTCATGGGGTCTTCTT----- 428
Qy      105 ThrHisAsnHisAsnHisProLeuLeuLysAspSerLeuSerSerThrLeuAlaCysIle 124
Db      429 -----CCTCATCAGTCCCCATTAAATAAGATATCTCTCTTCAACATTAGCATGTGTA 482
Qy      125 ValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPheIle 144
Db      483 CTTGCATTAACACGATGGAATGTTGGAAAGACCAAAATTAACAAAGTTTACATTACATT 542
Qy      145 GluSerAsnLeuAlaSerAlaThrGluLysSerGlnProSerProIleGlyPheAspIle 164
Db      543 GAGTCAAAATTTTGGCTTCAGTCACTGACAAAATCAAGCATCTCCCATTTGGTTTGCATC 602
Qy      165 IlePheProGlyLeuGluTrpAlaLysAsnLeuAspIleAsnLeuSerLysGln 184
Db      603 ATATTTCTGTGATGCTTGGATATGCAAAAGATTTGGATATAAATCCCTTTAAACCAA 662
Qy      185 ThrAspPheSerLeuMetLeuHisLysArgGluLeuGluGlnLysArgCysHisSerAsn 204
Db      663 ACACATTTGAGTGTGATGTTACATGAGAGAGAAATGGAGCTAAGAAGATGTCAATTCAAAT 722
Qy      205 GluMetAspGlyTyrrIleuAlaIleSerGluGlyLeuGlyAsnLeuTyrrAspTrpAsn 224
Db      723 GGGAGGGAAGCATCTTGGCATATATCTCAGAAGACCTTGGAAATTTAAATGACTGGAAC 782
Qy      225 MetValLysTyrrGlnMetLysAsnGlySerValPheAsnSerProSerAlaThrAla 244
Db      783 ATGGTATGAATATATCAATGAAGATGTTCTCTTTTCAACTCACCTCAGCAACAGCT 842
Qy      245 AlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrrLeuAsnSerLeuLeuAsp 264
Db      843 TCTGTCTTATTATCATCAATAAATGCTGGTTGTTCTTCTTCAATATCTAATCTCACTCTTGGAC 902

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QY 55 AnValGluIleSerValSerSerTyrAspThrAlaTyrValAlaMetValProSerPro 74
DB 228 AATGTTGAACCTTTCAATTTCTGCATATGATCTGCATGGGTGCAATGGTCTCTCCCA 287
QY 75 AnSerProLysSerProCysPheProGluCysLeuAsnTyrLeuIleAsnAsnGlnLeu 94
DB 288 AACTCTCTTAAATAAACCTCTTTTCTCGATGATGATAAATCTGGGTATAGATCATCAAAAC 347
QY 95 AnAspGlySerTyrGluValAsnHisThrHisAsnHisAsnHisProLeu---Leu 113
DB 348 CTGATGGGTCAATGGGCATCTC-----CATGACCATCAGTTGGTGATG 392
QY 114 LysAspSerLeuSerSerThrIleAlaCysIleValAlaLeuLysArgTyrAsnValGly 133
DB 393 AAAGCCACTCTCTTATCCACATTAGCATGTGTCTTACTCTTAAAGCATGGGATACGCT 452
QY 134 GluAspGlnIleAsnLysGlyLeuSerPheIleGluSerAsnLeuAlaSerAlaThrGlu 153
DB 453 GATGATCATATGAGCAAGGCCCTTAGTTTATCAAGTCTCAATATAGCTTCAGCTACTGAT 512
QY 154 LysSerGlnProSerProIleGlyPheAspIleIlePheProGlyLeuLeuGluTyrAla 173
DB 513 GAGATCAACGTTCTCTCTGGGATTTGACATAATTTTCTCTGGTATGATGATGCT 572
QY 174 LysAsnLeuAspIleAsnLeuSerLysGlnThrAspPheSerLeuMetLeuHisLys 193
DB 573 AAAGACTTGAATTTGAATCTAGCCCTGGCATCAATGAATGTGGATGCTTTGGTTCAAAAG 632
QY 194 ArgGluLeuGluGlnLysArgCysHisSerAsnGluMetAspGly-----TyrLeuAla 211
DB 633 AAAGAGTTGGAGCTTAGAAGCTGCTGTAGCAACTCTGAAGGAGGAAAACCTATTATAGCG 692
QY 212 TyrIleSerGluGlyLeuGlyAsnLeuTyrAspTyrAsnMetValLysLysTyrGlnMet 231
DB 693 TAGTTTTCAGAGGAATTCGAAATTTACAGACTGGGAATGGTCATGCGATCAAGG 752
QY 232 LysAsnGlySerValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGln 251
DB 753 AAGACGGATCACTGTGTAGTTCTCCATCCACCGCAGTGGCTTTTATGACACAGAAAT 812
QY 252 AsnProGlyCysLeuAsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValPro 271
DB 813 GATGATGGCTGTTTAAATTAACCTTCGCTCAGTCTTACAAAGTTTCATAGTTCAAGTTCCC 872
QY 272 ThrValTyrProHisAspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeu 291
DB 873 GCAATATATCTCTTGATATATGCTCGTTTACACATGTTGATAGCTTCAAAAACGTG 932
QY 292 GlyIleSerHisPheArgValGluIleLysAsnValLeuAspGluThrTyrArgCys 311
DB 933 GGGATTTGATGGCCATTTCAAGATGAGATTAGAAAGTGTATTAGATGAAACATACAGCTGT 992
QY 312 TrrValGluArgAspGluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg 331
DB 993 TGGATGCAAGGGAGGAAACATATTCTCAGATGCTTCAACTGTGCAATGGCTTCCCG 1052
QY 332 LeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu 351
DB 1053 ATGTACGTGTTCAGAGATATGATGTTTCTTCAGATCAATTCATCTCAGAGAGT 1112
QY 352 Leu-----AlaLeuLysAspGluTyrAlaAlaLeuGluThrTyr 364
DB 1113 CTCTTTTCAAAATTCCTCGAGGACATTTAAAGACTTTTAGTGCCTCACTAGAGTTATTT 1172
QY 365 HisAlaSerHisIleLeuTyrGlnGluAsp----- 374
DB 1173 AAGGCCCTCCAGATTAATATTTATCCGATGAGTTTATTCGGAAATATAAATCTCTGG 1232
QY 375 -----LeuSerSerGlyLysGlnIleLeuLysSerAlaAsp 386
DB 1233 ACTAGTCTGTTCTCTGAATCATGATTAATCTAGTGGT----- 1268

QY 387 PheLeuLysGluIleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGlu 406
DB 1269 -----TCAGTTCAATTCATGATAGAACTGAGAGACTCTGTGAAACAAGAG 1310
QY 407 ValGluAsnAlaLeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArg 426
DB 1311 GCAGTTAATGCTTTCGAGTTCCTCTATTAATCAACTCTGGAACGCTTATCAATAAGCGA 1370
QY 427 AsnIleGlnLeuTyrAsnValAspAsnThrArgIleLeuLysThrThrTyrHisSerSer 446
DB 1371 GCACCTGGAAGATTACAGTGGAGCATTTGTGAGGATTTTCAAAAACAGCATATGCTGCTTA 1430
QY 447 AsnIleSerAsnThrAspTyrLeuArgIleAlaValGluAspPheTyrThrCysGlnSer 466
DB 1431 AATTTTGGTCATCAAGATTTCTTGGAACTTGCTGTAGAGATTTCAATACCTGCAAGGC 1490
QY 467 IleTyrArgGluGluLeuLysGlyLeuGluArgTyrValValGluAsnLysLeuAspGln 486
DB 1491 ATACATCCGACGAACTGAAAGAGCTTGAAATAATGGTTCATCGAAACAATAATGGACAAG 1550
QY 487 LeuLysPheAlaArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSer 506
DB 1551 TTGAAATTTGCGAGACAGAAAGTTAGCGTACTGCTATTTTCTGCTGCAGCGACCTTAAC 1610
QY 507 SerProGluLeuSerAspAlaArgIleSerTyrAlaLysAsnGlyIleLeuThrThrVal 526
DB 1611 TCTCCAGAACTTTGATGCGCCGCTTATCATGGGCAAAAATGGGTATCTCACAAACCGTG 1670
QY 527 ValAspAspPhePheAspIleGlyGlyThrIleAspGluLeuThrAsnLeuIleGlnCys 546
DB 1671 GTTGATGATTTCTTGTGTTGAGGAGCTGGAAGAGGAATTCGTAAACCTTATACAATTG 1730
QY 547 ValGluLysTyrAsnValAspValAspLysAspCysCysSerGluHisValArgIleLeu 566
DB 1731 GTGAAAAGTGGGATGCCAGTGGCAACCGGTTACTGTTCACAGAGGCTTGAGATTATA 1790
QY 567 PheLeuAlaLeuLysAspAlaIleCysTyrIleGlyAspGluAlaPheLysTyrGlnAla 586
DB 1791 TTTCTTGCACTTCATAGCACAATTTGTGAAATAGGAAAAAAGCTTTACTTGGCAAGGA 1850
QY 587 ArgAspValThrSerHisValIleGlnThrTyrLeuGluLeuMetAsnSerMetLeuArg 606
DB 1851 CCACGGTGTAGGAAATGTTATCCATATTTGGTTGGCTTCGCTCGAGTCAATGAGGAAG 1910
QY 607 GluAlaIleTyrThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAla 626
DB 1911 GAAGCTGAATGCTTGAATAAAGTAGTGCATCATTCGATCGATACATGGAATAATGGC 1970
QY 627 TyrValSerPheAlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLys 646
DB 1971 TATGATATCATTTGCTTTGGGACCTATAGTCTTCCAAACGCTCTACTTTTGTGACCTAAG 2030
QY 647 LeuSerGluGluIleValGluSerSerGluTyrHisAsnLeuPheLysLeuMetSerThr 666
DB 2031 CTTCCAGAGAAATTTGTTGAAATTTGTGAATACAGAACTCTTTAAGCTGATGAGCACT 2090
QY 667 GlnGlyArgLeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeu 686
DB 2091 TCTGGCCGCTCTTCAATCATCTCGAACTTTTGTAGAGAGTCCACAGCGAAGGAAATTA 2150
QY 687 AsnAlaValAlaLeuHisLeuSerAsnGlyGluSerGlyLysValGluGluValVal 706
DB 2151 AATGCTTGTCTCTATACATGATTAGTCCGGTGTGAAGCTCACCAGAGGAGGAGCCACT 2210
QY 707 GluGluMetMetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGlu 726
DB 2211 GAAGCAATGAAGGAGATGTTGATAGGACAGAGAGAACTGTTGAGATTAGTTTTCAG 2270
QY 727 GluAsnGlySerIleValProArgAlaCysLysAspAlaPheTyrAsnMetCysHisVal 746
DB 2271 GAGAAC--AGTACAATTTCCAAGAGCTTGTAAAGGATTTTCTCTGGAATAATGAGCTGT 2327
QY 747 LeuAsnPhePheTyrAlaAsnAspAspGlyPheThrGlyAsnThrIleLeuAspThrVal 766


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Db 2328 GTGCATCTATTATTTACAGGAAGATGATGGTTTACATCCCATGATGATGAACCTCTGCG 2387
Qy 767 LysAspIleIleTyrAsnProLeuValLeu 776
Db 2388 AAAGCCTTATTGGAACAACCCATGGTGTCTG 2417

RESULT 5
US-10-041-018-378
; Sequence 378, Application US/10041018
; Publication No. US2004007232A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 378
; LENGTH: 2658
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Coding
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2658)
; OTHER INFORMATION: Coding
US-10-041-018-378

Alignment Scores:
Pred. No.: 1.05e-187 Length: 2658
Score: 2023.50 Matches: 393
Percent Similarity: 69.1% Conservative: 150
Best Local Similarity: 50.0% Mismatches: 212
Query Match: 49.2% Indels: 31
DB: 7 Gaps: 8

US-10-041-018-383 (1-784) x US-10-041-018-378 (1-2658)
Qy 16 AsnArgProAlaAlaLeuSerAlaIleHisThrAlaSerThrSerHisGlyGlnThr 35
Db 147 TCCCGACCTACCGCGGTGCGCCGTTTGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 206
Qy 36 AsnProThrAsnLeuIleAspThr----- 44
Db 207 CTATTCCTCGAGTGGATGGGACACACAACTAAACTGGAGCTTTGCACTTTTGAAGAA 266
Qy 45 ThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSerValSerSerThrAsp 64
Db 267 ACAAAAGAAAGAAATTAAGAAATGTTTCGACAAAGGTTGAACCTTTCAGTTCTGCAATATGAT 326
Qy 65 ThrAlaTTPValAlaMetValProSerProAsnSerProLysSerProCysPheProGlu 84
Db 327 ACTGCAAGGTGGCAATGGTCTCTCTCCAACTCTCTCAACCAACCTCTTTTCCCGAG 386
Qy 85 CysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHis 104
Db 387 TGATATAAATCGGTATAGATAGTCAACATGCTGATGGCTCATGGGCGCTACTC----- 440
Qy 105 ThrHisAsnHisAsnHisProLeuLeu---LysAspSerLeuSerSerThrLeuAlaCys 123
Db 441 -----CACAAACCATCAGTTGCTGATGAAGGCCAACTCTTATCTACATTAGCATGT 491
Qy 124 IleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPhe 143
Db 492 GTTCTTACTCTTAAGCGGTGGAATATTGGGCATGATCATATGACGAAGGCCCTTGATTTT 551
Qy 144 IleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnProSerProIleGlyPheAsp 163
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Db 552 ATCAAGTCTAATATAGCTTCAGCTACTGATGAGAACCAACGTTCTCCGGTGGGATTGAC 611
Qy 164 IleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsnLeuSerLys 183
Db 612 ATTATTTTCCCTGGCATGATTGATGATGCTTAAAGACTTGAATTTGAATTCACCCCTTGCA 671
Qy 184 GlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGlnLysArgCysHisSer 203
Db 672 CCGACGAACGCTGGATGCCTTGGTTCCGAAGAAGAGTTGGAGCTGAGAAGCTGCAGNAGC 731
Qy 204 AsnGluMetAspGly-----TyrLeuAlaTyrIleSerGluGlyLeuGlyAsnLeuTyr 221
Db 732 AACTCTGAAGGTGGAAGAGCCTATTATTAGCGTATGTTTCAGAAGAAATTCGAAAGTTACAG 791
Qy 222 AspTTPAsnMetValLysLysTyrGlnMetLysAsnGlySerValPheAsnSerProSer 241
Db 792 GACTGGGATATGGTCATGCAATATCAAGGAAGAAATGGATCCTGTTTAAATTCCTCATCC 851
Qy 242 AlaThrAlaAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrLeuAsnSer 261
Db 852 ACTACGGCAGCGCTTTTATGTCATAGAAATGATGATGGCTGTTTGTATATCTTCGCTCA 911
Qy 262 LeuLeuAspLysPheGlyAsnAlaValProThrValTyrProHisAspLeuPheIleArg 281
Db 912 CTCTTACAAAAGTTTGCATGGCTCAGTTCACATATATATCTCTGATATATATGCTCGA 971
Qy 282 LeuSerMetValAspThrIleGluArgLeuGlyIleSerHisIlePheArgValGluIle 301
Db 972 TTACACATGGTTGATAGCCTTCAAAATTCGGAATTCGCGCATTTCAAAGAGGAGATT 1031
Qy 302 LysAsnValLeuAspGluThrTyrArgCysTrpValGluArgAspGluGlnIlePheMet 321
Db 1032 AGNAGGTATTAGTCAAACTTACAGGTGTTCGATCGAAGGAGGAAATATATATTCTTA 1091
Qy 322 AspValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsnGlyTyrGluValSer 341
Db 1092 GATGCTTCAACTTGTCAATGGCCTTTCGAATGTTACGTGTTGCAAGGATATGATGTTCT 1151
Qy 342 ProAspProLeuAlaGluIleThrAsnGluLeu-----AlaLeu 354
Db 1152 TCAGACCAGTTCGACTCAATTTTCAGAAAGATATCTTTCCCAATTCCTTCGAGGATATTA 1211
Qy 355 LysAspGluTyrAlaAlaLeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAsp 374
Db 1212 AAAGACTTCGTCGCTCGCTGGAGTTATATAGGCTCTCAGATTATACGCAACCCGAT 1271
Qy 375 LeuSerSerGlyLysGlnIleLeuLys---SerAlaAspPheLeuLysGluIleSer 393
Db 1272 GAATCTGTTCTGGAATAATATAAATCTTCGACTAGTCTGTTCTGGAAGCATGATATCT 1331
Qy 394 ThrAsp-----SerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
Db 1332 AGTGATTCAGTTTGGTCTGATAGACCGGATAGTGTGTTTAAACCAAGAGGCTGTATAATGCT 1391
Qy 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
Db 1392 CTGTAGTTCCTCTATTAATGCAACTCTAGAACCGCTTAATAGTAAGAGGCAATGGAAAGT 1451
Qy 431 TyrAsnValAspAsnThrArgIleLeuLysThrTyrHisSerSerAsnIleSerAsn 450
Db 1452 TACAGTGGAGACATTGTGAGGATTTCAAATTCGCCATATGCTCTGCTTAAATTTTGGCCAT 1511
Qy 451 ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu 470
Db 1512 CAAGATTTTCTGGAACCTTCGTAGAGGATTTCAATACCTCGCAACCGCATTCATCTTAA 1571
Qy 471 GluLeuLysGlyLeuGluArgTrpValValGluAsnLysLeuAspGlnLeuLysPheAla 490
Db 1572 GAACTGGAAAGAGCTTCAAAGATGGGTGGTTGAAACAAATTTGACGAGTTGAAATTTTC 1631
Qy 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
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Db 1632 AGACTGCACCTAGGCTACTCTATTTTGTCTGGCGAGCGACCTTACTGATCCTGAACCTT 1691
Qy 511 SerAspAlaArgIleSerTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhe 530
Db 1692 CATGATGCTCGCATAGCATGGGCACAAATGGTGTCTCACCAGCCGTGTGATGATTC 1751
Qy 531 PheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrp 550
Db 1752 TATGATGGTGGAGGATCTCAAGAGGAATTTGGATAACCTTTATAGAAATTTGGTGGAAAGTGG 1811
Qy 551 AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
Db 1812 GATCTGATGGGAAGTGGTGTACTGTTCCAGGAGCTTGAGATGTGATTTCTTGCACTG 1871
Qy 571 LysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThr 590
Db 1872 CACAGCACAGTTTGTGAATAGGAAGAGAGCTTTAGTAGTGGCAAGGACGAGTGTATG 1931
Qy 591 SerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrp 610
Db 1932 AGGAATGTTATCGATGTTGGTGGTCTGCTGCTGAAGGTGATGAGAAGGAAGCTGAATGG 1991
Qy 611 ThrArgAspAlaTyrrValProThrLeuAsnGluTyrrMetGluAsnAlaTyrrValSerPhe 630
Db 1992 TCGACAAATAAGGTAGTGCATCAATGGGTGAATATATGGAACAAGCCCATGTATCATTC 2051
Qy 631 AlaLeuGlyProIleValLysProAlaIleTyrrPheValGlyProLysLeuSerGluGlu 650
Db 2052 GCGTTGGGACCTATAATCTCTCAATGCTCTCTTTGTTGGACCTAAACTCTCAGAGGAA 2111
Qy 651 IleValGluSerSerGluTyrrHisAsnLeuPheLysLeuMetSerThrGlnGlyArgLeu 670
Db 2112 ATGATTTGGAAGCTGTGAATACCAAGAGTTATATAGCTGATGAGCACTGCTGTCGCCTT 2171
Qy 671 LeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValAla 690
Db 2172 AAGAATGATTCGATCTTACGATAGAGAAATGCAAGAGGGAAGCTGAATATTCGTCT 2231
Qy 691 LeuHisLeuSerAsnGlyGluSerGlyLysValGluGluGluValValGluMetMet 710
Db 2232 CTGTGATGATTCATGCGCGTGTGTAATGTCCACCAAGAGAGGCCCATTCAGCAATATAA 2291
Qy 711 MetMetIleLysAsnLysArgLysGluLeuMetLysLeuPheGluGluAsnGlySer 730
Db 2292 GGGGATTTTCAGAGGGCGGATAAGAGAGCTGCTGGGTTAGTTTTCAGGAGAAC---ACT 2348
Qy 731 IleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePhe 750
Db 2349 ACAATTTCCAAGAGCTTGTGAAGGATTTGTTCTGGAATTTGATGTCCATTGTGAATCTAATT 2408
Qy 751 TyrAlaAsnAspAspGlyPheThrGlyAsnThrIleLeuAspThrValLysAspIleIle 770
Db 2409 TACATGGAAGATGATGGGTACACTTCAATAGTTGATGACACTGTAAAAGCCATGTTT 2468
Qy 771 TyrAsnProLeuValLeu 776
Db 2469 GAACAACCCATGGATCTG 2486
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RESULT 6

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US-10-041-018-381
; Sequence 381, Application US/10041018
; Publication No. US2004007232A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080051/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 381
; LENGTH: 2658
; TYPE: DNA
; ORGANISM: Cucurbita maxima
US-10-041-018-381

Alignment Scores:
Pred. No.: 1,05e-187 Length: 2658
Score: 2023.50 Matches: 393
Percent Similarity: 69.1% Conservative: 150
Best Local Similarity: 50.0% Mismatches: 212
Query Match: 49.2% Indels: 31
DB: 7 Gaps: 8

US-10-041-018-383 (1-784) x US-10-041-018-381 (1-2658)
Qy 16 AsnArgProAlaAlaLeuSerAlaIleHisThrAlaSerThrSerHisGlyGlnThr 35
Db 147 TCCCGACCTACCGCGGTGGCCGTTTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 206
Qy 36 AsnProThrAsnLeuIleIleAspThr----- 44
Db 207 CTATTTCCCTGGAGTGGATGTGGACACAACTAAAACTGGAGCTTTGCACTTTGAAGAA 266
Qy 45 ThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSerValSerSerTrpAsp 64
Db 267 ACAAAAGAAAGAAATTAAGAAATTTTCGACAAAGGTGAACCTTTCAGTTTCTGCATATGAT 326
Qy 65 ThrAlaTrpValAlaMetValProSerProAsnSerProLysSerProCysPheProGlu 84
Db 327 ACTGATGCGTGGCAATGGTCTCTCTCCAACTCTCTCAACCAACCTCTTTTCCCGAG 386
Qy 85 CysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHis 104
Db 387 TGTATAAACTGGTATTAGATAGTCAACATGCTGATGGCTCATGGGCTCTACTC----- 440
Qy 105 ThrHisAsnHisAsnHisProLeuLeu---LysAspSerLeuSerSerThrLeuAlaCys 123
Db 441 -----CACACGATCAGTTGCTGATGAAGGCCAATCTCTTATCTACATTAGCATGT 491
Qy 124 IleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPhe 143
Db 492 GTTCTTACTCTTAAAGCGGTGGATATTTGGCGATGATCATATGAGCAAGCCCTTGATTTT 551
Qy 144 IleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnProSerProIleGlyPheAsp 163
Db 552 ATCAAGTCTAATAGCTTCAGCTACTGATGAGAACCAACGTTCTCCGCTGGGATTTGAC 611
Qy 164 IleIlePheProGlyLeuGluTyrrAlaLysAsnLeuAspIleAsnLeuSerLys 183
Db 612 ATTATTTTCCCTGGCATGATGATGATGCTAAAGACTTGAATTTGAATCTACCTTTGGCA 671
Qy 184 GlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGluGlnLysArgCysHisSer 203
Db 672 CCGACGACGCTGGATGCTGGTTCCAAAGAAAGTTGGAGCTGAGAGCTGCAGAACG 731
Qy 204 AsnGluMetAspGly-----TyrLeuAlaTyrrIleSerGluGlyLeuGlyAsnLeuTyrr 221
Db 732 AACTCTGAAGGTGGAAGCCCTATTAGCGTATGTTTCAGAAAGGAATTCGAAAGTTACAG 791
Qy 222 AspTrpAsnMetValLysLysTyrrGlnMetLysAsnGlySerValPheAsnSerProSer 241
Db 792 GACTGGGATATGCTCATGCAATATCAAGAGAAATGGATCACTGCTTTTAATTTCTCCATCC 851
Qy 242 AlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrrIleLeuAsnSer 261
Db 852 ACTACGGCAGCGCTTTTATGATAGAAATGATGATGCTGTTTGTGATTTATCTTCCTCA 911
Qy 262 LeuLeuAspLysPheGlyAsnAlaValProThrValTyrrProHisAspLeuPheIleArg 281
Db 912 CTCCTTACAAAAGTTTGGTGGCTCAGTTCCCAATATATATCTCTTGTATATATATGCTCGA 971
Qy 282 LeuSerMetValAspThrIleGluArgLeuGlyIleSerHisHisPheArgValGluIle 301
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Db 1603 GTGGTTGATGACTCTTCGATGTTGGTGATCAAAAGAAAGAAATTAGAAACCTGATAGCA 1662
Qy 546 CysValGluLeuYrTrpAsnValAspValAspLysAspCysCysSerGluHisValArgile 565
Db 1663 CTAGTTGAGAAATGGCATCGCACCATGAGTTGAGTTCTATTTCGGAACAGGTGAAATA 1722
Qy 566 LeuPheLeuAlaLeuLysAspAlaLeuCysTrpIleGlyAspGluAlaPheLysTrpGln 585
Db 1723 GTATTTCTGCTATTATACAACAGTGAACCATCTTTGGAGCAATGGCTTCTGCAGCACAA 1782
Qy 586 AlaArgAspValThrSerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeu 605
Db 1783 GCGCGTGATCTTACAAACCACTAGTAGAATAATGGCTGGATTTGTTAGATCTATGATG 1842
Qy 606 ArgGluAlaIleTrpThrArgAspAlaTrpValProThrLeuAsnGluTrpMetGluAsn 625
Db 1843 GTCGAGGCAGAAATGGCAGAGATGCCAATATGTACCAACAGTTTGAAGAATACATGACAAT 1902
Qy 626 AlaTrpValSerPheAlaLeuGlyProIleValLysProAlaIleTrpPheValGlyPro 645
Db 1903 GCTGTTGTCTCATTTGCACTGGGCCCAATTTGTCTCCACGACATTTGATTTTGTAGGGCAA 1962
Qy 646 LysLeuSerGluGluIleValGluSerSerGluTrpHisAsnLeuPheLysLeuMetSer 665
Db 1963 GAGCTATTAGAGATGCTGTCAAGATGAAGATGACATAAATTATTTAGGCTATGAGC 2022
Qy 666 ThrGlnGlyArgLeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLys 685
Db 2023 ACTTCGGCGAGGCTCTCAATGACTACCAAAAGTTTAGAGAGGGAGGCAACAGGGGAG 2082
Qy 686 LeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSerGlyLysValGluGluVal 705
Db 2083 CTGAATAGTGTCTCTACTTGTCTCCACAGTGGTGGTCTCTATGTCTCCATAGAAGCCGCT 2142
Qy 706 ValGluGluMetMetMetMetLysAsnLysAsnLysArgLysGluLeuMetLysLeuIlePhe 725
Db 2143 AAAAGGCAATCAGAAAGTCCATAGACGTCTAGAGAGACATTCGTAAGATGTTCTTC 2202
Qy 726 GluGluAsnGlySerIleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHis 745
Db 2203 AGGAAGAA--AGTCTGTTCTTAGGCCATGCAAGGACCTCTCTGGAAGATGTTAAG 2259
Qy 746 ValLeuAsnPhePheTrpAlaAsnAspAspGlyPheThrGly--AsnThrIleLeuAsp 764
Db 2260 ATACTTCACTGTTTACTCTCAGAATGATGGATTAGCTCCCAAGGAAATGGTCACT 2319
Qy 765 ThrValLysAspIleLeuTrpAsnProLeuValLeuValAsn 778
Db 2320 GCAGTGAATGCTGTTATCAACGAGGCCACTCAAAAGTCCAAAT 2361
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RESULT 9

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US-10-425-115-22041
; Sequence 22041, Application US/10425115
; Publication No. US2004021472A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 22041
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MMT4577_120098C.1
; US-10-425-115-22041
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Alignment Scores:
Pred. No.: 9.51e-153 Length: 2716
Score: 1668.00 Matches: 351
Percent Similarity: 62.0% Conservative: 141
Best Local Similarity: 44.2% Mismatches: 260
Query Match: 40.6% Indels: 42
DB: 8 Gaps: 9
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US-10-041-018-383 (1-784) x US-10-425-115-22041 (1-2716)

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Qy 7 IleAlaSerProLeuLeuThrLysSerAsnArgProAlaAlaLeuSerAlaIleHisThr 26
Db 114 CTGGTGCTCTGATGCTATCTGATTCCTTTCTTCCACAGCGTATGCCAGAGCGGTG 173
Qy 27 AlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleAspThrThrLys 46
Db 174 GTTGCAGAAAAC-----ACAAGCCTGCCAAACATGCATAGAAGAACTTGAG 221
Qy 47 GluArgIleGlnLysGlnPheLysAsnValGluIleSerValSerSerTyrAspThrAla 66
Db 222 ACTATAATAAGGAATCAGCTCCGGAAGCCCACTTGTGCCACCTTCTTCATACGACACAGCG 281
Qy 67 TrpValAlaMetValProSerProAsnSerProLysSerProCysPheProGluCysLeu 86
Db 282 TGGGTTTCTATGTCGCCAGTGGCGGGCTCTCATCAGACTCCCGCTTCCACAGTGTGT 341
Qy 87 AsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHisThrHis 106
Db 342 GAGTGGATATTGCAGAAATCAGCAGGATGATGATCTTGGGGTGTG-----AGC 389
Qy 107 AsnHisAsnHisProLeuLeuLysAspSerLeuSerSerThrLeuAlaCysIleValAla 126
Db 390 CAATCTGACTCATCTCGCTCAGCAAGGATGTTCTCTATCCACGTTGGCATGTGTCTTGGCG 449
Qy 127 LeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLysSerPheIleGluSer 146
Db 450 TTGAAGAGATGAATGTTGGCAGAGAGAAACATTTGGAGAGGACTGCATTTTCATCGGAGG 509
Qy 147 AsnLeuAlaSerAlaThrGluLysSerGlnProSerProIleGlyPheAspIlePhe 166
Db 510 AATTTCTCTGTTGCTATGACACCAGCAGTTCACTTCTCTATAGTTTCAACATCACCTTT 569
Qy 167 ProGlyLeuLeuGluTrpAlaLysAsnLeuAspIleAsnLeuSerLysGlnThrAsp 186
Db 570 CCTGTTTCTTAACTCGGCATTTGATATGGGTTTAGAATTTCTCTGTAAAGACAACTGAT 629
Qy 187 PheSerLeuMetLeuHisLysArgGluLeuGlnLysArgCysHisSerAsnGluMet 206
Db 630 GTCTGTGGCATTTCTTACCGCCGGGAGATGGAAATTTGAAAAGGCTGGCTGTGATAGTTCT 589
Qy 207 AspGly-----TyrLeuAlaTrpLysSerGlyLeuGlyAsnLeuTrpAspTrp 223
Db 690 TTTTGAAGAAAAGCATATATATGCTTTTATCCAGAAAGGATTCGGAATATATGCTGGACTGG 749
Qy 224 AsnMetValLysTrpGlnMetLysAsnGlySerValPheAsnSerProSerAlaThr 243
Db 750 GATCAAGTTTATGAAGTTTCAGAGGAAGAATGGATCATTTTCAGCAGCTCTCTTCCCAACT 809
Qy 244 AlaAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTrpLysAsnSerLeuLeu 263
Db 810 GCTGTTGCAATTATCCAAATAACACGACCAAGCCCTTCAATACCTAATATTTGCTTGTTC 869
Qy 264 AspLysPheGlyAsnAlaValProThrValTrpProHisAspLeuPheIleArgLeuSer 283
Db 870 AGTGAATTTGGCAGTGCAGTACCAAGATGATCTCTTCAATGGTATACATGTGTCAGCTTCA 929
Qy 284 MetValAspThrIleGluArgLeuGlyLysSerHisHisPheArgValGluIleLysAsn 303
Db 930 ATGGTGGAGCGCTTTGAAAAAATGGGAATTTCTCAGCGCTTTGTCAAGTGAATAGAAAGC 989
Qy 304 ValLeuAspGluThrTrpArgCysTrpValGluArgAspGluGlnIlePheMetAspVal 323
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Db 990 ATCTGGACATGGCATCAAAATGCTGTTACAGAAAGATGAGAAATCATGATGACATA 1049
 QY 324 ValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsnGlyTyrGluValSerProasp 343
 Db 1050 GCAACATGTCATGGCATTCGCTTTGAGGATGAATGTTACAAATGTTCTCTCAGAT 1109
 QY 344 ProLeuAlaGluIleThrAsnGluLeuAlaLeuLysAspGluTyrAlaAlaLeuGluThr 363
 Db 1110 GAGCTGCTCAGCTT-----GCTGGAGCTTCCACT 1139
 QY 364 TyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSer----- 377
 Db 1140 TTCATGATTCATACAGGATATTTAAATGATACAAAATCCCTACTGGAATTTGACAAG 1199
 QY 378 ---GlyLysGlnIleLeuLysSerAlaAspPheLeuLysGluIleLeuSerThrAspSer 396
 Db 1200 ACCTCAAAAGTCACCTTATCAGAAACGATCTGATCTTAGATCGCATAGGTTCTGCTCT 1259
 QY 397 AsnArgLeuSerLys-----LeuIleHisLys 405
 Db 1260 GGCACACTATTGAAGGATAGATGCTGTAGTAGGTGCAAAAGACTCGATTTTGGGA 1319
 QY 406 GluValGluAsnAlaLeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArg 425
 Db 1320 GAGATGGAGTATGCTGTTAAATTTCCCTTGTATTCACACTGGAGCGCTTAGAACACAAG 1379
 QY 426 ArgAsnIleGlnLeuTyrAsnValAspAsnThrArgIleLeuLysThrThrTyrHisSer 445
 Db 1380 AGAAACATCAACAATTTGATGCTTGGGGTCTCTGATGCTA---ACAAACAAATCTCTCA 1436
 QY 446 SerAsnIleSerAsnThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGln 465
 Db 1437 TCTTTTCGTATCATCAAGAAATTCCTAGCTTGGCAGTCGAAGATTCAGTTCTCTCAA 1496
 QY 466 SerIleTyrArgGluGluLeuLysGlyLeuGluArgTyrValValGluAsnLysLeuAsp 485
 Db 1497 CGTGTTCGCGGATGAATTCGCGCATCTTGATAGTTGGGTGAAGGAGAACAAAGCTGGAC 1556
 QY 486 GlnLeuLysPheAlaArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeu 505
 Db 1557 CAGCTACAATTTGCTGGCAGAACTGACATATTTGCTATCTGCTGCTGCTGCTACCGTA 1616
 QY 506 SerSerProGluLeuSerAspAlaAlaArgIleSerTyrAlaLysAsnGlyIleLeuThrThr 525
 Db 1617 TTTTCTCTGAATGCTGACGCTCGCATTTTCATGGCCAAAATGGTGTCTCTCACAACT 1676
 QY 526 ValValAspAspPhePheAspIleGlyGlyThrIleAspGluLeuThrAsnLeuIleGln 545
 Db 1677 GTGGTTGATGACTTCTTCGATGTTGGTGGATCAAAAGNAGATTAGAAAACCTGATAGCA 1736
 QY 546 CysValGluLysTyrAsnValAspValAspLysAspCysCysSerGluHisValArgIle 565
 Db 1737 CTAGTTGAGAAATGGCATGCGCACCATCGCATGTTGAGTTCTATTTCGGAACAGGTGAATA 1796
 QY 566 LeuPheLeuAlaLeuLysAspAlaIleCysTyrIleGlyAspGluAlaPheLysTyrGln 585
 Db 1797 GTATTTTCTCTATTATATACACAGTGAACCATCTTGGACATGCGCTTCGACAGACAA 1856
 QY 586 AlaArgAspValThrSerHisValIleGlnThrTyrPheGluLeuMetAsnSerMetLeu 605
 Db 1857 GGCCTGTGATCTTACAAACACCATCTAGTAGAAATATGGCTGGATTTGTTAAGATCTATGATG 1916
 QY 606 ArgGluAlaIleTyrThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsn 625
 Db 1917 GTCGAGGACAAATGGCAGATGCCAATATGTATGTACCAACAGTTTGAAGAATAATCATGACAAAT 1976
 QY 626 AlaTyrValSerPheAlaLeuGlyProIleValLysProAlaIleTyrPheValGlyPro 645
 Db 1977 GCTGTGTCTATTGCACTGGGCCCAATTTGCTCCACACATTTGATTTTGTAGGCA 2036
 QY 646 LysLeuSerGluGluIleValGluSerSerGluTyrHisAsnLeuPheLysLeuMetSer 665
 Db 2037 GAGCTATTAGAGCATGCTGTCAAAGATGAAGATGACGATAAATATTATTAGGCTAGTGAGC 2096

QY 666 ThrGlnGlyArgLeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLys 685
 Db 2097 ACTTGGGAGGGCTCTCTCAATGACTACCAAAAGTTTAGAGAGGAGCAACACCGGGAAG 2156
 QY 686 LeuAsnAlaValAlaLeuHisLeuSerAsnGlyLysSerGlyLysValGluGluVal 705
 Db 2157 CTGAATAGTGTCTTCTACTTGTGCTCCACAGTGGTGTCTATGTCATAGAAGCGCT 2216
 QY 706 ValGluGluMetMetMetMetMetMetMetMetMetMetMetMetMetMetMetMet 725
 Db 2217 AAAAGGCAATGCAAGAGTCCATAGACGCTCTAGGAGACACTTCTAAGATTGGTCTC 2276
 QY 726 GluGluAsnGlySerIleValProArgAlaCysLysAspAlaPheTyrAsnMetCysHis 745
 Db 2277 AGGAAGAA---AGTCTGTCTTAGGCCATGCAAGAGCTCTTCTGGAAGATGTGTAA 2333
 QY 746 ValLeuAsnPhePheTyrAlaAsnAspAspGlyPheThrGly---AsnThrIleLeuAsp 764
 Db 2334 ATACTTCACCTGTTTACTCTCAGATGATGATTTAGTCTCCCAAGAAATGGTCAGT 2393
 QY 765 ThrValLysAspIleIleTyrAsnProLeuValLeuValAsn 778
 Db 2394 GCAGTGAATGCTCTGTTATCAACGAGCCACTCAAAATGCTCAAAAT 2435

RESULT 10

US-10-425-115-22042
 ; Sequence 22042, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(5322)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 22042
 ; LENGTH: 2730
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRF4577_120099C.1
 US-10-425-115-22042

Alignment Scores:
 Pred. No.: 3 84e-147 Length: 2730
 Score: 1611.00 Matches: 346
 Percent Similarity: 62.4% Conservative: 143
 Best Local Similarity: 44.1% Mismatches: 249
 Query Match: 39.2% Indels: 46
 DB: 8 Gaps: 10

US-10-041-018-383 (1-784) x US-10-425-115-22042 (1-2730)

QY 35 ThrAsnProThrAsnLeuIleAspThrThrLysGluArgIleGlnLysGlnPheLys 54
 Db 290 ACAAGCTGCGCAACATGATAGGAAGATCTTGAGACTATAAAGGAATCAGTCCGG 349
 QY 55 AsnValGluSerValSerSerTyrAspThrAlaTyrValAlaMetValProSerPro 74
 Db 350 AAGCCCAAGTTGCCACTTCTTCATACGACACAGCGTGGTGTCTATGGTCCAGTCCGG 409
 QY 75 AsnSerProLysSerProCysPheProGluCysLeuAsnTyrLeuIleAsnAsnGlnLeu 94
 Db 410 GGCTCTCATCAGACTCCCGCTCCACAGTGTGTGATGGATATCTGCAGACACAGCAG 469
 QY 95 AsnAsp-GlySerTyrGlyLeuValAsnHisThrHisAsnHisAsnHisProLeuLeu 114
 Db 470 GATGATGGGATCTTGGGTGTC-----AGCCAATCTGACTCATCGTCCAGCAA 517

QY 114 sAspSerLeuSerSerThrLeuAlaCysIleValAlaLeuLysArgTrpAsnValGlyCl 134
 Db 518 GGATGTTCTCCATCCACGCTGGCATGTGTTCTGCGTTGAAGAGATGAATGTTGGCAG 577
 QY 134 uAspGlnIleAsnLysGlyLeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLys 154
 Db 578 AGAGAACATTTGGAGAGAGCTGCAATTTCACTCGGAGGAATTTCTGTGCTATGGACGA 637
 QY 154 sSerGlnProSerProIleGlyPheAspIleIle-PheProGlyLeuLeuGluTrp-Ala 173
 Db 638 GCAGTTCACTCTCCATAGGTTCAACTTCACTTCTGTTGTTGTTGCTTCCGCA 697
 QY 174 LysAsnLeuAspIleAsnLeuSerLysGlnThrAspPheSerLeuMetLeuLys 193
 Db 698 TTTGATATGGGTTAGAAATTTCTGTAAGACAACTGATGCTGTGGCATTTCTTCCCGC 757
 QY 194 ArgGluLeuGluGlnLysArgCysHisSerAsnGluMetAspGly-----TyrLeu 210
 Db 758 CGGGAGATGGAAATTTGAAAGGCTGGCTGTGGATAGTTCTTTTGGAGAAAGCATATATG 817
 QY 211 AlaTyrIleSerGluGlyLeuGlyAsnLeuTyrAspTrpAsnMetValLysLysTyrGln 230
 Db 818 GCTTTTATCCAGAGGATTCGGAAATATGCTGGACTGGGATCAAGTTTATGAAGTTTCAG 877
 QY 231 MetLysAsnGlySerValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHis 250
 Db 878 AGGAAGATGGATCATTTGTTTCAGCATCTCCACAACTGCTGTTGCATTAATCCACAA 937
 QY 251 GlnAsnProGlyCysLeuAsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaVal 270
 Db 938 TCAACAGCAAGCCCTTCAATACCTAAATTTGCTTGTCAAGTAAATTTGGCAGTGCAGTA 997
 QY 271 ProThrValTyrProHisAspLeuPheIleArgLeuSerMetValAspThrIleGluArg 290
 Db 998 CCAGCAATGTATCTTCATGTGTACATGCTCAGCTTCAATGGTGGCGCTTGAANA 1057
 QY 291 LeuGlyIleSerHisPheArgValGluIleLysAsnValLeuAspGluThrTyrArg 310
 Db 1058 ATGGGAATTTCTCAGCGCTTGTGAGTGAATAGAAAGCATCTCGACATGCATACAA 1117
 QY 311 CysTrpValGluArgAspGluGlnIlePheMetAspValValThrCysAlaLeuAlaPhe 330
 Db 1118 TGTGTTTACAGAAAGATGAGGAATCATGTGGACATAGCAATGTGCAATGGCATTT 1177
 QY 331 ArgLeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsn 350
 Db 1178 CGCCTTTTCAGGATGAATGTTTACAAATGTTCTTCAGATGAGTGTCTCACGTTGCTGA 1237
 QY 351 GluLeuAla-----LeuLysAspGluTyrAlaAlaLeuGlu 362
 Db 1238 GCTTCCACTTTCCATGATTCACATCAAGGATATTTAAATGATACAAAATCCCTACTGGA 1297
 QY 363 ThrTyrHisAlaSerHisIle---LeuTyrGlnGluAspLeuSerSerGlyLysGlnIle 381
 Db 1298 TTGTACAGACCTCAAAAGTCACCTTTATCAGAAACGATCTGATCTTAGATCGCATAGT 1357
 QY 382 LeuLysSerAlaAspPheLeuLys----- 389
 Db 1358 TCCTGCTCGGCACTTATTTGAAGGATAGATGTGCTGTAGTGGTGCAAAAGACTCG 1417
 QY 390 -----GluIleIleSerThr-AspSerAsn-----ArgLeuSerLysLeuIle 403
 Db 1418 ATTTTGGAGAGGTGCTGCAAAACAAATTTAAATTTCTCACTTTTCCACGGGAGTTTCAGT 1477
 QY 403 eHisLys-----GluValGluAsnAlaLeuLysPheProIleAsnThrGln 418
 Db 1478 TTATGTCTGTGTTTGTGATTTTCAGATGAGATGCTGTGTAATTTTCCCTTGTATTTCCAC 1537
 QY 418 YLeuGluArgIleAsnThrArgArgAsnIleGlnLeuTyrAsnValAspAsnThrArgIle 438
 Db 1538 ACTGGAGCGCTAGACACACAGAGAAACATCGAACATTTTGTGCTTGGGTTCTCTGAT 1597

QY 438 eLeuLysThrThrTyrHisSerSerAsnIleSerAsnThrAspTyrLeuArgLeuAlaVa 458
 Db 1598 GCTA---ACAAACAAATCTCTCATCTTTTCGTATCAATCAAGAAATTCCTAGCTTTGGCAGT 1654
 QY 458 lGluAspPheTyrThrCysGlnSerIleTyrArgGluGluLeuLysGlyLeuGluArgTr 478
 Db 1655 CGAAGATTTCAAGTTCTCTCTCAACGTTGTTTACCGGATGAACCTTCGGCATCTTGATAGTTG 1714
 QY 478 pValValGluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThrAlaTyrCysTy 498
 Db 1715 GGTGAAGGAGAACAAAGCTGGACAGCTACATTTGCTCGCAGAAACTGACATATTGCTA 1774
 QY 498 rPheSerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaAaXileSerTrpAl 518
 Db 1775 TCTGTCTGCTGCTGCTACCGTATTTTCTCTGAATTTGCTGACGCTCGCATTTTCATGGGC 1834
 QY 518 aLysAsnGlyIleLeuThrThrValValAspAspPhePheAspIleGlyGlyThrIleAs 538
 Db 1835 CAAAATGGTGTCTCCACAACTGTGTTGATGACTTCTTCGATGTTGGTGGATCAAAAGA 1894
 QY 538 pGluLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAspLysAspCy 558
 Db 1895 AGAATTAGAAAACCTGATAGCACTAGTTGAGAAATGGCATGGCCACCATGCGATTTAGATT 1954
 QY 558 sCysSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGl 578
 Db 1955 CTATTTCGAACAGGTGAAAATAGTATTTCTCTATTTATATACACAGTGAACCATCTTGG 2014
 QY 578 YAspGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGlnThrTrpLe 598
 Db 2015 AGCAATGCTTCTGCGACGACGCGTGATCTTACAAACCATCTAGTAGAATAATGGCT 2074
 QY 598 uGluLeuMetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyrValProTh 618
 Db 2075 GGATTTGTTAAGATCTATGATGCTCGAGCAGAAATGGCAGATGCGCAATATGTATCAAC 2134
 QY 618 rLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIleValLysPr 638
 Db 2135 AGTTGAAGAAATACATGACAAATGCTGTTGTCATTTGACCTGGGCCCAATTTGTCTCC 2194
 QY 638 oAlaIleTyrPheValGlyProLysLeuSerGluLulleValGluSerSerGluTyrHi 658
 Db 2195 AGCATTTGATTTTGTAGGCAAGAGCTATTAGAGCATGCTGTCAAAGATGAAGAGTACGA 2254
 QY 658 sAsnLeuPheLysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIleHisSerPheLy 678
 Db 2255 TAAATTTATTTAGCTAGTGCACACTTGGCGGAGGCTCCTCAATGACTACCAAGTTTGA 2314
 QY 678 sArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSe 698
 Db 2315 GAGGGAAGCAACCCAGGGGAAGCTGAATAGTGTGTTCTTACTTGTGCTCCACAGTGGTG 2374
 QY 698 rGlyLysValGluGluValValGluGluMetMetMetIleLysAsnLysArgLy 718
 Db 2375 TTTATGTTCCATAGAACCGCTAAAAGGCAATGCAGAGATCCATAGAGTGTCTAGGAG 2434
 QY 718 sGluLeuMetLysLeuIlePheGluAsnGlySerIleValProArgAlaCysLysAs 738
 Db 2435 AGACTTGTCTAGATTTGTTCTCAGAAAAGAA---AGTGTGTTTCTTAGGCCATGCAAGGA 2491
 QY 738 pAlaPheTrpAsnMetCysHisValLeuAsnPhePheTyrAlaAsnAspAspGlyPheTh 758
 Db 2492 GCTCTTCTGGAAGATGTGTAAAGATCTTCACTGTTTACTCTCTCAGAAATGATGATTTAG 2551
 QY 758 rGly---AsnThrIleAspThrValLysAspIleIleTyrAsnProLeuValLeuVa 777
 Db 2552 CTCCTCCAAAGGAATGGTCAGTGCAGTGAATGCTGTATCAACGAGCCACTCAAGTCCA 2611
 QY 777 lAsn 778
 Db 2612 AAAT 2615

RESULT 11


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QY 439 ulysThrThrTyT----- 443
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QY 444 -----HisSer-Ser----- 446
D 45139 TGGCAGCCAGCTTCCATTAAACGACATCTAATCAGGGCATTCATCTCTCATCTTGT 45080
QY 447 -----AsnIleSerAsnThrAspTyrIleuArgLeuAlaValG 459
D 45079 TTCTTCTGTGTCTAGTTTGGCAATATTTGCACCTCTCATATCTCTGAAGTTAGTGTGG 45020
QY 459 luaspPheTyrThrCysGlnSerIleTyrArgGluLeuLysGlyLeuGlu----- 476
D 45019 ATGACTTCAATTTTGCAGCTCCATACACCGTGAAGAAATGAACGCTCTGTAGTGTGG 44960
QY 476 ----- 476
D 44959 CTCCAGCTAAGCTTTTTCATTTATTCAGCCTTCTTGCATTAAGCTAATTTAGTTTACTTA 44900
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D 44899 TATATAACACACACTTGAACGAGTTTCAGTTTAAATTCAGGTGTGACTTCTATTTGTT 44840
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D 44839 ATGTAGTCACAATTCAGCAATGCTGCTACCAACTTTCAGAGTGGATTTGGGAGATAGAT 44780
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D 44779 TGCAGGAACCTGAATTTTGCAGACAGACTGGCTTACTGTATTCTCTGGGGCTGCAA 44720
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QY 524 hrThrValValAspAspPheAspIleGlyThrIleAspGluLeuThrAsnLeu 544
D 44659 CAACGGTGTAGACGACTTCTTTGTATGTTGGAGGGTCCAAAGAAAGACTGGAACCTCA 44600
QY 544 leGlnCysValGluLysTrpAsnValAsp----- 553
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D 44482 TGTT-CCTGAGTACAGCTCAGAACATGTTTGAGATCATATTTCTCAGTTCTTAAGGGACACCA 44424
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QY 594 leGln----- 595
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QY 596 -----Thr-TrpLeuGluLeuMetAsn 602
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QY 603 SerMetLeuArgGluAlaIleTrpThrArgAspAlaTyrValProThrLeuAsnGluTyr 622
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QY 623 MetGluAsnAlaTyrValSerPheAlaLeuGlyProIleValLysProAlaIleTyrPhe 642
D 44183 ATGGAATGCGTACATATCATTTGATTTAGGACCAATTTGCTCCAGCTACCTATCTG 44124
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QY 677 ----- 677
D 44004 CTTAAATCTCAAACTTTTACTAACTGTACAGTTGAAAGATGGCAAGAGCCCTAAA 43945
QY 677 ----- 677
D 43944 TCCAACAAATTAATGGTAATTAACAACTCTGCTCATAGATTTCGGATTATATATCCCT 43885
QY 678 -----LysArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHis 692
D 43884 TTTGATGTTTTTTCGAGAGAGAAAGCGCGAAGGAGCTGAATCGCGTTCATTGCAC 43825
QY 693 LeuSerAsnGlyLysSerGlyLysValGluGluValValGluGluMetMetMet 712
D 43824 ATGAACACGAGAGAGACAATCGCAGCAAGAAAGTGTATAGAAATCGAATGAAAGTTTA 43765
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D 43704 CCAAGGGAATGCAAGAGCGTTCTTGAAATGAGCAAGTGTGAACTTATTTACAGG 43645
QY 753 AsnAspAspGlyPheThrGlyAsnThrIleLeuAspThrValLysAspIleIleTyrAsn 772
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QY 773 ProLeuValValAsnGluAsn 780
D 43584 CTTGTAGCTTACAGAGAAATCT 43561
RESULT 12
US-10-259-194A-107
; Sequence 107, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Chassemian, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 70029-NP
; CURRENT APPLICATION NUMBER: US/10/259,194A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,743
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 107
; LENGTH: 2223
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-194A-107
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934	Db	ATGGCATTTTCGTATGTTGGTATGAATGGATATGATGTTTCTTCCAGATGAGCTATCTCAT	993
348	Qy	IleThr-----AsnGluLeuAla-----LeuIysAspGluTyrAla	359
994	Db	TTTTCTGAAACCTTCAAAGTTTCCAAATTCATTCAAAGGATATCTCGAATGATGACAAGATCT	1053
360	Qy	AlaLeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLys	379
1054	Db	TTATTAGATTACATTAATGAGCTTCAAAGTC-----	1083
380	Qy	GlnIleLeuLysSerAlaAspPheLeuLysGluIleIleSerThrAspSerAsnArgLeu	399
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400	Qy	SerLysLeuIleHisLysGluValGluAsnAlaLeuLysPheProIleAsnThrGlyLeu	419
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420	Qy	GluArgIleAsnThrArgArgAsnIleGlnLeuTyrAsnValAspAsnThrArgIleLeu	439
1141	Db	GATCGCTGACCATTAAGAANAATCGAAATTTTGACATTTACACGAGTCAGATGCTA	1200
440	Qy	LysThrThrTyrHisSerSerAsnIleSerAsnThrAspTyrLeuArgLeuAlaValGlu	459
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460	Qy	AspPheTyrThrCysGlnSerIleTyrArgGluGluLeuLysGlyLeuGluArgTrrPheVal	479
1258	Db	GATTTTAGTAGCTCTCAGTTTATTTTCCAAAGAGAGCTGCAGCAACTCAACAGCTGGGTG	1317
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1498	Db	CTGAAACACCTCTGCGCATTTAGTTGAGAGTGGGCAAGAATGACAAAACCTGAGTACTAC	1557
560	Qy	SerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAsp	579
1558	Db	TCGTGAACAGTAGAGATTGTTTCTCTGCAATTTATCTTCAACTAACCCAGCTTGGATCA	1617
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600	Qy	LeuMetAsnSerMetLeuArgGluAlaIleTrrThrArgAspAlaTyrValProThrLeu	619
1678	Db	TTCTCAGGTCATTATGATGACAGAGGTAGAGTGGAGCGAGCCGGTATGTGCCAACAGCA	1737
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1798	Db	TTGTATCTTGTGGACCAAGATCCCTGATTCTGTCTATAAGAACCAAGAAATGCGACGAG	1857
660	Qy	LeuPheLysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIleHisSerPheLysArg	679
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 QY 510 LeuSerAspAlaArgLysThrAlaLysAsnGlyLysLeuThrThrValValAspAsp 529
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 QY 530 PhePheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLys 549
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 QY 590 ThrSerHis-ValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAla1 609
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 QY 609 eTrpThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValse 629
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 QY 728 AsnGlySerIleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeu 747
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 QY 748 AsnPhePheTyrAlaAsnAspAspGlyPheThrGlyAsnThrIleLeuAspThrValLys 767
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 QY 768 Asp---IleIleTyrAsnProLeuValLeu 776
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RESULT 14

US-10-425-114-5988
 ; Sequence 5988, Application US/10425114
 ; Publication No. US2004003488A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 5988
 ; LENGTH: 2029
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700550363_FLI
 US-10-425-114-5988

Alignment Scores:

Pred. No.: 2,07e-120 Length: 2029
 Score: 1337.00 Matches: 280
 Percent Similarity: 62.6% Conservative: 116
 Best Local Similarity: 44.2% Mismatches: 198
 Query Match: 32.5% Indels: 39
 Gaps: 7

US-10-041-018-383 (1-784) x US-10-425-114-5988 (1-2029)

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 QY 203 SerAsnGluMetAspGly-----TyrLeuAlaTyrIleSerGluGlyLeuGlyAsn 219
 Db 84 GTGGATAGTCTTTTGGAGAAAGCATATATGGCTTTTATCCCAAGAGGATTCGGAAT 143
 QY 220 LeuTyrAspTrpAsnMetValLysLysTyrGlnMetLysAsnGlySerValPheAsnSer 239
 Db 144 ATCTGGACTGGGATCAAGTATGAGTTTCAGAGGAGAAATGATCATCTTTTTCAGCACT 203
 QY 240 ProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLysLeuAsnTyrLeu 259
 Db 204 CCTTCACAACTGCTGTGTCATTTAATCCACAAATACACGACCAAGCCTTTCAATACCTA 263
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 QY 340 ValSerProAspProLeuAlaGluIleThrAsnGluLeuAla----- 353
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GenCore version 5.1.7
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Run on: February 16, 2006, 06:52:12 ; Search time 383.242 Seconds
(without alignments)
3636.365 Million cell updates/sec

Title: US-10-041-018-383

Perfect score: 4113

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Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2023.5	49.2	2658	3	US-08-727-308-3
3	1523	37.0	2403	3	US-09-614-912-23
4	1084.5	26.4	2705	3	US-10-041-007-1
5	1075	26.1	2388	3	US-10-041-007-36
6	1075	26.1	2445	3	US-10-041-007-34
7	1075	26.1	2622	3	US-10-041-007-32
8	1062.5	25.8	2861	3	US-09-398-395A-55
9	1062.5	25.8	2861	3	US-09-887-586A-55

Sequence 55, Appl
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Sequence 3, Appl
Sequence 38, Appl
Sequence 1, Appl
Sequence 43, Appl
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Sequence 14, Appl
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Sequence 37, Appl
Sequence 13, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-727-308-2
; Sequence 2, Application US/08727308
; Patent No. 6020176
; GENERAL INFORMATION:
; APPLICANT: YUJI KAMIYA et al.
; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,308
; FILING DATE: October 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850


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Db 1992 TCACAAATAAGTAGTGCATCAATGGGTGAATATATATGACCAAGCCCATGTATCATTC 2051
Qy 631 AlaLeuGlyProIleValIysProAlaIleTyrPheValGlyProIleValSerGluGlu 650
Db 2052 GCCTTGGGACCTAATATCTTCCCAATGCTCTCTTTTGGACCTAAACTCTCAGAGGAA 2111
Qy 651 IleValGluSerSerGluTyrHisAsnLeuPheLysLeuMetSerThrGlnGlyArgLeu 670
Db 2112 ATGATTGGAAGCTGTGAATACCAAGAGTATATATAGCTGATGAGCACTGCTGCTGCCCTT 2171
Qy 671 LeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValAla 690
Db 2172 AAGAATGATATTCGATCTTACGATAGAGATGCAAGAGGGAAGCTGAATATTCGTCT 2231
Qy 691 LeuHisLeuSerAsnGlyGluSerGlyLysValGluGluValValGluGluMetMet 710
Db 2232 CTGTGATGATTGCGGTGGTGAATGTCAACCAAGAGAGGCCATTGAAGCAATATAA 2291
Qy 711 MetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlySer 730
Db 2292 GGGGATTTGAGAGGGGATAGAGAGCTCTCGGGTTAGTTTTCAGGAGAAC---ACT 2348
Qy 731 IleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePhe 750
Db 2349 ACAATTCGAAGAGCTTGTAAGGATTTCTCGGAATTTGATGCTCATTTGTAATCTATT 2408
Qy 751 TyrAlaAsnAspAspGlyPheThrGlyAsnThrIleLeuAspThrValLysAspIleIle 770
Db 2409 TACATGGAAGATGATGGTACACTTCAAAATAGTGTGATGAACACTGTAAAAGCCATGTT 2468
Qy 771 TyrAsnProLeuValLeu 776
Db 2469 GAACAACCCATGGATCTG 2486

RESULT 2
US-08-727-308-3
; Sequence 3, Application US/08727308
; Patent No. 6020176
; GENERAL INFORMATION:
; APPLICANT: YUJI KAMIYA et al.
; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,308
; FILING DATE: October 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2658 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-727-308-3

Alignment Scores:
Pred. No.: 4,61e-220 Length: 2658
Score: 2023.50 Matches: 393
Percent Similarity: 69.1% Conservative: 150
Best Local Similarity: 50.0% Mismatches: 212
Query Match: 49.2% Indels: 31
DB: 3 Gaps: 8

US-10-041-018-383 (1-784) x US-08-727-308-3 (1-2658)
Qy 16 AsnArgProAlaAlaLeuSerAlaIleHisThrAlaSerThrSerHisGlyGlnThr 35
Db 147 TCCCGACCTACCGCGCTTGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 206
Qy 36 AsnProThrAsnLeuIleIleAspThr----- 44
Db 207 CTATTCCTCCGTGGAGTGGATGTGGACACACAACTAAACTGGAGCTTTGCATTTGAAGAA 266
Qy 45 ThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSerValSerSerTyrAsp 64
Db 267 ACNAAAGAAGAATTAAGAAATTTGTCGACAGGTTGAAGTTTCACTTTCTGATATGAT 326
Qy 65 ThrAlaTrpValAlaMetValProSerProAsnSerProLysSerProCysPheProGlu 84
Db 327 ACTGCATGGTGGCAATGGTTCCTCTCCAAACTCTCTCAACCAACCTCTCTTTCCCGAG 386
Qy 85 CysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHis 104
Db 387 TGTATAAACTGGGTATTAGATAGTCAACATGCTGATGGCTCATGGGCGCTTACTTC- 440
Qy 105 ThrHisAsnHisAsnHisProLeuLeu---LysAspSerLeuSerSerThrLeuAlaCys 123
Db 441 -----CACACGATCAGTTGCTGATGAAGGCCAATCTCTTATCTACATTAGCATGT 491
Qy 124 IleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPhe 143
Db 492 GTTCTTACTCTTAAGCGGTGAATATTTGGCATGATCATATGACGAAGGCCCTTGATTTT 551
Qy 144 IleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnProSerProIleGlyPheAsp 163
Db 552 ATCAAGTCTAATATAGTCTCAGCTACTGATGACCAACCAAGTCTCCGGTGGGATTTGAC 611
Qy 164 IleIlePheProGlyLeuLeuGluTyrAlaLysAsnLysAspIleAsnLeuLeuSerLys 183
Db 612 ATATTTTTCCTGGCATGATTGATGATGATGATGATGATGATGATGATGATGATGATGATG 671
Qy 184 GlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGluGlnLysArgCysHisSer 203
Db 672 CCGACGACGCTGGATGCTTGGTTCGAAAGAAAGAGTGGAGCTGAGAGCTCAGAGAGC 731
Qy 204 AsnGluMetAspGly-----TyrLeuAlaTyrIleSerGluGlyLeuGlyAsnLeuTyr 221
Db 732 AACTCTGAAGGTGGAAAGCCCTATTTAGCGTATGTTTTCAGAGGAATTTGGAAGTTACAG 791
Qy 222 AspTrpAsnMetValLysLysTyrGlnMetLysAsnGlySerValPheAsnSerProSer 241
Db 792 GACTGGATATGTCATGCAATATCAAGAGAGATGATGATGATGATGATGATGATGATGATG 851
Qy 242 AlaThrAlaAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrLeuAsnSer 261
Db 852 ACTACGGCAGCGCTTTTATGTCATAAATGATGATGATGATGATGATGATGATGATGATG 911
Qy 262 LeuLeuAspLysPheGlyAsnAlaValProThrValTyrProHisAspLeuPheIleArg 281
Db 912 CTCTTACAAAAGTTTTCATGCTCAGCTTCCCAACAATATATCTCTTATATATATGTCGA 971
Qy 282 LeuSerMetValAspThrIleGluArgLeuGlyIleSerHisIlePheArgValGluIle 301
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Db 972 TTACACATGGTGTAGAGCTTCAAAATTCGGAAATTCGCGCAATTTCAAAGAGAGATT 1031
Qy 302 LysAsnValLeuAspGluThrTyrArgCysTrpValGluArgAspGluGlnIlePheMet 321
Db 1032 AGAAGCGTATTAGATGAACCTTACAGGTGTGGATCGAAGGAGAGAAATATATTCTTA 1091
Qy 322 AspValValThrCysAlaIleAlaPheArgLeuLeuArgIleAsnGlyTyrGluValSer 341
Db 1092 GATGCTTCAACTGTGCAATGGCTTTCGAATGTACGTGTGAAGGATGATGATGTTC 1151
Qy 342 ProAspProLeuAlaGluIleThrAsnGluLeu-----AlaLeu 354
Db 1152 TCAGACCACTTGACTCAATTTTCAGAGATATCTTTCCCAATTCCTCGAGGATATTTA 1211
Qy 355 LysAspGluTyrAlaAlaLeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAsp 374
Db 1212 AAAGACTTCGGTGCCTCGCTGGAGTTATATAGGCTCTCAGATTATACGCCACCCGAT 1271
Qy 375 LeuSerSerGlyLysGlnIleLeuLys---SerAlaAspPheLeuLysGluIleSer 393
Db 1272 GAATCTGTTCTCGAAATATAAAGCTTCGACCTAGTCGTTTCTCGAAGCATGGATTATCT 1331
Qy 394 ThrAsp-----SerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
Db 1332 AGTGATTCAGTTGCTGCTAGAACCGATAGTGTGTGTTAAACAGAGAGCTGTATAGCT 1391
Qy 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
Db 1392 CTTGAGTTCCTTAAATCACTAGAACGCCATAAGTAAGTAGAGGCCAATGGAAAGT 1451
Qy 431 TyrAsnValAspAsnThrArgIleLeuLysThrTyrHisSerSerAsnIleSerAsn 450
Db 1452 TACAGTGGAGACATGTGAGGATTTCAAATCGCCATATCGCTGCTTAAATTTTGCCCAT 1511
Qy 451 ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu 470
Db 1512 CAAGATTTCTGGAATCTGCTGAGAGGATTTCAATACCCTGCACCGCAATCATCTTAA 1571
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Db 1572 GAACTGGAAGAGCTTCAAAGATGGGTGGTTGAAACAAATTCGACGATGAAATTTTTC 1631
Qy 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrIleuSerSerProGluLeu 510
Db 1632 AGACTGCACCTAGGGTACTGCTATTTGCTGGCGACGACCTTACTGATCCTGAACTT 1691
Qy 511 SerAspAlaArgIleSerTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhe 530
Db 1692 CATGATGCTCGATAGCATGGGCACAAATGGTGTGCTCACACCGTGGTTGATGATTC 1751
Qy 531 PheAspIleGlyGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrp 550
Db 1752 TATGATGGTGGAGGATCTCAAGAGGAATTCGATAACCTTATAGAATTGGTGAAAGTGG 1811
Qy 551 AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
Db 1812 GATCCTGATGGGAAGATGGGTACTGTTCCAAAGGAGCTTGAGATTGTATTTCTGCACTG 1871
Qy 571 LysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThr 590
Db 1872 CACAGCACAGTTTGTGAATAGAGAGAGCTTTAGTAGGCAAGGACGCGAGTGTATG 1931
Qy 591 SerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrp 610
Db 1932 AGGAATGTTATCGATGGTTGGTCTGCTGCTGAAGGTGATGAGAAAGCAAGCTGAATGG 1991
Qy 611 ThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPhe 630
Db 1992 TCGACAAATTAAGGTAGTGCATCATGCGGTGATATATATGGAACCAAGCCCATGTATCATTC 2051
Qy 631 AlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLysLeuSerGluGlu 650

Db 2052 GGGTTGGGACCTATAATCCTTCCATGCTCTCTTTTGGACCTAAACCTCTCAGAGGAA 2111
Qy 651 IleValGluSerSerGluTyrHisAsnLeuPheLysLeuMetSerThrGlnGlyArgLeu 670
Db 2112 ATGATTTGGAAGCTGTGAATACCAGAGATATATAAGCTGATGAGCACTCTCGTCGCTT 2171
Qy 671 LeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValAla 690
Db 2172 AAGATGATATTCGATCTTCATGATAGAAATCCAAAGAGGGAAGCTGAATATTCGTCT 2231
Qy 691 LeuHisLeuSerAsnGlyLysSerGlyLysValGluGluValValGluGluMetMet 710
Db 2232 CTGTGCGATTTGATGGCGGTGTAATGTCCACAAAGAGAGGCCATTGAAGCAATATA 2291
Qy 711 MetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlySer 730
Db 2292 GGGGATTTTGAGAGGCGCATTAAGAGAGCTGCTGGGGTTAGTTTTCAGGAGAAC---ACT 2348
Qy 731 IleValProArgAlaCysLysAspAlaPheTyrAsnMetCysHisValLeuAsnPhePhe 750
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Qy 751 TyrAlaAsnAspAspGlyPheThrGlyAsnThrIleLeuAspThrValLysAspIleIle 770
Db 2409 TACATGGAAGATGATGGGTACACTTCAAATAGTTGATGAACACTGTAAAGCCATGTT 2468
Qy 771 TyrAsnProLeuValLeu 776
Db 2469 GAACAACCCATGGATCTG 2486

RESULT 3
US-09-614-912-23
; Sequence 23, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Cai, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 23
; LENGTH: 2403
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1049)
US-09-614-912-23
Alignment Scores:

Pred. No.: 5,54e-163 Length: 2403
 Score: 1523.00 Matches: 317
 Percent Similarity: 62.1% Conservative: 133
 Best Local Similarity: 43.7% Mismatches: 233
 Query Match: 37.0% Indels: 42
 DB: 3 Gaps: 8

US-10-041-018-383 (1-784) x US-09-614-912-23 (1-2403)

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 DB 12 CTCAGAACCCAGCAGGATGATGATCTTGGGGTGC-----AGCCAATCTGAC 59
 QY 110 HisProLeuLeuLysAspSerLeuSerThrLeuAlaCysIleValAlaLeuLysArg 129
 DB 60 TCATCGGTGACAGGATGATCTTCCATCCACGTTGGCATGTGTTCTTGGGTTGAAGA 119
 QY 130 TrpAsnValGluAspGlnIleAsnLysGlyLeuSerPheIleGluSerAsnLeuAla 149
 DB 120 TGGAAATGTTGGCAGAGAGAACATTTGGAGAGGACTGCATTTTCATCGGGAGGAATTTCTCT 179
 QY 150 SerAlaThrGluLysSerGlnProSerProIleGlyPheAspIleIlePheProGlyLeu 169
 DB 180 GTTGCTATGACGACGAGTTCATCTCTCTATAGGTTCAACTTTCACCTTCTCTGGTTTG 239
 QY 170 LeuGluTyrrAlaLysAsnLeuAspIleAsnLeuLeuSerLysGlnThrAspPheSerLeu 189
 DB 240 CTTAGCTCGGCATTGATGGGTGTAGAAATTCCTGTAGACAAATTTGATGTCTGGC 299
 QY 190 MetLeuHisLysArgGluLeuGluGlnLysArgCysHisSerAsnGluMetAspGly--- 208
 DB 300 ATTCTTTCACGCGCGGAGATGGAATTCGAAAGGCTGGCTGGATAGTCTCTTTTGGAGA 359
 QY 209 -----TyrLeuAlaTyrrIleSerGluGlyLeuGlyAsnLeuTyrrAspTrpAsnMetVal 226
 DB 360 AAAGCATATATGCTTTTATCCAGAGGATGCGAAATATGCTGGAGTGGATCAAGTT 419
 QY 227 LysLysTyrrGlnMetLysAsnGlySerValPheAsnSerProSerAlaThrAlaAla 246
 DB 420 ATGAGTTTCAGAGGAGATGATGATCTTCCAGACTCTTCCCAACTGCTGTGCA 479
 QY 247 PheIleAsnHisGlnAsnProGlyCysLeuAsnTyrrLeuAsnSerLeuLeuAspLysPhe 266
 DB 480 TTAATCCACAAATACACAGCAGCCCTCAATACCTAAATTTGCTTGTCAATGAATTT 539
 QY 267 GlyAsnAlaValProThrValTyrrProHisAspLeuPheIleArgLeuSerMetValAsp 286
 DB 540 GGCAGTGCAGTACCAATGATATCTTCAAGGGGTACATTTGTCAGCTTTCAATGGTGGAC 599
 QY 287 ThrIleGluArgLeuGlyIleSerHisPheArgValGluIleLysAsnValLeuAsp 306
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 DB 660 ATGCATACAAATGCTGGTTACAGATGATGAGAACTCATGATGATGACATGCAATTT 719
 QY 327 AlaLeuAlaPheArgLeuLeuArgIleAsnGlyTyrrGluValSerProAspProLeuAla 346
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 QY 347 GluIleThrAsnGluLeuAla-----LeuLysAspGluTyrr 358
 DB 780 CAGCTTGTGGAGCTTCCATTTCCATGATCTACAGGATATTTAAATGATACAAA 839
 QY 359 AlaAlaLeuGluThrTyrrHisAlaSerHisIle---LeuTyrrGlnGluAspLeuSerSer 377
 DB 840 TCCCTACTGGAATTTGACAGACCTCAAAAGTCACTTATCAGAAACGATCTGATCTTA 899
 QY 378 GlyLysGlnIleLeuLysSerAlaAspPheLeuLysGluIleIleSerThrAspSerAsn 397
 DB 900 GATCGCATAGGTTCTCGCTGGCAACTTATTTGAAGGATAAGATGTGCTGTAGAGGTG 959

QY 398 ArgLeuSerLysLeuIleHisLys-----GluValGluAsnAlaLeuLysPhePro 405
 DB 960 CAAAAGACTCGATTTTGGAGAGATGCTGCAACAAAATTTAAATCTCTATTTTACCTT 1019
 QY 406 -----GluValGluAsnAlaLeuLysPhePro 414
 DB 1020 GGAGGTTTCAGTTTATGCTGTGTTTGTGTTTTCAGATCAGTATGCTGTAAATTTTCCC 1079
 QY 415 IleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeuTyrrAsnValAsp 434
 DB 1080 TTGATTTCCACCTGGAGCGCTAGAACACAGAGAAACATCAAGCAATTTTGTATGCTTGG 1139
 QY 435 AsnThrArgIleLeuLysThrTyrrHisSerSerAsnIleSerAsnThrAspTyrrLeu 454
 DB 1140 GGTTCCTCTGATGCTA--ACAACAAAATCTCATCTTTTCGTATCATCAAGAATTTCTTA 1196
 QY 455 ArgLeuAlaValGluAspPheTyrrCysGlnSerIleTyrrArgGluGluLeuLysGly 474
 DB 1197 GCTTTGGCAGTCCGAAGATTTTCAGTTCTCTCAACGTTTACCGGGATGAATTCGGCAT 1256
 QY 475 LeuGluArgTrpValValGluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThr 494
 DB 1257 CTTGATGTTGGTGAAGGAGAACAGCTGGACGACTCAATTTGCTCGGCAAACTG 1316
 QY 495 AlaTyrrCysTyrrPheSerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArg 514
 DB 1317 ACATATTTGCTATCTGCTGCTGCTACCGTATTTTCTCTGAATTTGCTGACGCTCGC 1376
 QY 515 IleSerTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhePheAspIleGly 534
 DB 1377 ATTTTCATGGCCAAAATGTTGCTCTCAACCTGCTGATGATGATCTTCTCGATGTTGGT 1436
 QY 535 GlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspVal 554
 DB 1437 GGATCAAAAGAAATTTAGAAAACCTGATAGCACTAGTTGAGAAATGGCATGGGACCAT 1496
 QY 555 AspLysAspCysCysSerGluHisValArgIlePheLeuAlaLeuLysAspAlaIle 574
 DB 1497 GCAGTTGAGTTCTATTTCGACAGGTGAAATAGTATTTTCTGCTATTATACACAGTG 1556
 QY 575 CysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIle 594
 DB 1557 AACCATCTGGAGCAATGCTTCTGCAGCACAAAGCGCTGATCTTACAAACCACTAGTA 1616
 QY 595 GlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAla 614
 DB 1617 GAAATGCTGGATTTGTTAAGATCTATGATGCTGAGGCAAGATGGCAGAGATGCCAA 1676
 QY 615 TyrValProThrLeuAsnGluTyrrMetGluAsnAlaTyrrValSerPheAlaLeuGlyPro 634
 DB 1677 TATGTACCAACAGTTGCAAGNATACATGACAAATGCTGTTGCTCAITTTGCTGGGCCCA 1736
 QY 635 IleValIleProAlaIleTyrrPheValGlyProLysLeuSerGluGluIleValGluSer 654
 DB 1737 ATTGTCTCCAGCATTTGTTATTTAGGGCAAGAGCTATTAGAGCATGCTGTCAAGAT 1796
 QY 655 SerGluTyrrHisAsnLeuPheLysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIle 674
 DB 1797 GAAGATACGATAAATTTATTTAGGCTAGTAGCAGCTTGGGGAGGCTCTCAATGATAC 1856
 QY 675 HisSerPheLysArgGluPheLysGluLysLeuAsnAlaValAlaLeuHisLeuSer 694
 DB 1857 CAAAGTTTAGAGGAGGAGCAACACAGGGGAGCTGAAATAGTGTCTCTACTTGTGCTC 1916
 QY 695 AsnGlyGluSerGlyLysValGluGluValValGluGluMetMetMetMetIleLys 714
 DB 1917 CACAGTGGTGGTCTTATGTCATAGAAAGCGCTGAAAGCAAGATGCAGAGTCCATAGAC 1976
 QY 715 AsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlySerIleValProArg 734
 DB 1977 GTGCTAGAGGAGACTTGTAAAGTTGGTTCCTCAGGAAAGAA---AGTGTGTTCTTAGG 2033
 QY 735 AlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePheTyrrAlaAsnAsp 754


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QY 496 TyxCysTyrPheSerValAlaLaThrLeuSerSerProGluLeuSerAspAlaArgile 515
Db 1796 GAAATGTTATTTCTCAGTGGCGTTAGTATGTTTGGAGCCAGAAATTCGCTGCTTGTAGAATT 1855
QY 516 SerTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhePheAspIleGlyGly 535
Db 1856 GCCTATGCCAGACTCTCTCCCTGCGCAGTATTTCTAGACGATCTTTACGACACCCACGGA 1915
QY 536 ThrIleAspGluLeuThrAsnLeuLeuGlnCysValGluLysTrpAsnValAspValAsp 555
Db 1916 TCCTGTGATGATCTTAATATGTTCTCTGAAGCGTCCGAAGATGGGATATCTCTGTGCTG 1975
QY 556 LysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCys 575
Db 1976 GATAGCGTTCCGGGATATCAGTTGAAAGTTTGTCTCTAGGGCTGTACACACACAGTGAAT 2035
QY 576 TrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGln 595
Db 2036 GGATTTGGAAAGATGACTCAAGGAACAAGCGCGTGTATGCTGGGCTATCTTTCGAAAA 2095
QY 596 ThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyr 615
Db 2096 GTATGGAGGGCTGTCTCGCATGCTATACCAAGAGCCGAATGTCGGCAGCAAGTAT 2155
QY 616 ValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIle 635
Db 2156 GTCCGACATTCACGAATATGTGGAATGCCAAAGTGTCCATAGCACTTGGCAGCAGTC 2215
QY 636 ValLysProAlaIleTyrPheValGlyProLysLeuSerGluGluIleValGluSerSer 655
Db 2216 GTACTAACTCAATCTTTTCACTGGGAGAAATTAATCTCTGATTAATTTTACAGCAAGTA 2275
QY 656 GluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIle 674
Db 2276 GACCTCGGTCGCAAAATTTCTGCATCTTGTGCTTTGTACTGACGACTAATCAATGACACC 2335
QY 675 HisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSer 694
Db 2336 AAGACTTACCAGCCGAGAGAAACCGTGGTGAATTTGTTTCCAGCGTACAGTG-CTACAT 2394
QY 695 AsnGlyGluSerGlyLys-ValGluGluGluValValGluGluMetMetMetMetIleLy 714
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Db 2455 CAACGCGACTGAAGAAATG---AATTGGGAGTTGGCCAAACCCAGCGAGCAATGCCCAT 2511
QY 734 GAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePheTyrAlaAsnAs 754
Db 2512 GTGTGTGAGAGACTGCTGTTCAACACTGCAAGAGTGATGCAGCTGTTTATATGTACAG 2571
QY 754 pAspGlyPhe-----ThrGlyAsnThrIleLeuAs 764
Db 2572 AGATGGCTTTGGTATCTCTGACAAAGAGATGAAAGACCATGTGACGCCGAATCTTTTCCA 2631
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RESULT 5

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US-10-041-007-36
; Sequence 36, Application US/10041007
; Patent No. 6946283
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; PRIOR FILING DATE: 2001-01-05
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; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 2388
; TYPE: DNA
; ORGANISM: Ginkgo biloba
US-10-041-007-36
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Alignment Scores:
Pred. No.: 7 93e-112 Length: 2388
Score: 1075.00 Matches: 261
Percent Similarity: 52.1% Conservative: 157
Best Local Similarity: 32.5% Mismatches: 332
Query Match: 26.1% Indels: 54
DB: 3 Gaps: 13
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US-10-041-018-383 (1-784) x US-10-041-007-36 (1-2388)

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Db 22 CCAGCTGTCTGGAAGGACGATTTTCATCGACTCTCTAACATCCCTTAATTCACGCGACA 81
QY 30 SerHisGlyGlyGlnThrAsnProThrAsnLeuIleAspThrThrLysGluArgIle 49
Db 82 TCGAAATCAAGCGTCGATGAGACAATCAATAAAAGAAATCCAGACATTTGGTGAAGAAATC 141
QY 50 GlnLysGlnPheLysAsnVal-----GluIleSerValSerSerTyrAspThrAla 66
Db 142 CAGTGCATGTTTCAGTCCATGCGGCGGAGCGGTGAACGAATCCATCTGCATATGATACAGCT 201
QY 67 TrpValAlaMetValProSerProAsnSerProLysSerProCysPheProGluCysLeu 86
Db 202 TGGGTGGCAAGATTCGTCATTTGACGGCTCTGCTGCACCCCAATTTTCCCAACCGTT 261
QY 87 AsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHisThrHis 106
Db 262 CAATGGATTTCTGAACAATCAATCAATGCGCAGATGGCTCGTGGGT----- 303
QY 107 AsnHisAsnHisProLeuLeuLysAspSerLeuSerSerThrLeuAlaCysIleValAla 126
Db 304 GAGGAGTGCAATTTTCTGGCGTATGACAGATTTTAAACACTCTCGCTCGCTCCTCACT 363
QY 127 LeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPheIleGluSer 146
Db 364 CTCAAATATGGAATAAGGCGGACATTCAGTGCAGAAAGGGGTGAGTTTGTGAGAAA 423
QY 147 AsnLeuAlaSer---AlaThrGluLysSerGlnProSerProIleGlyPheAspIleIle 165
Db 424 CACATGGAAGAAATGAAGGACGAAAGCTGACAATCACAGGCCAAGTGGATTCGAGGTCTG 483
QY 166 PheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsnLeuSerLysGlnThr 185
Db 484 TTTCTTGCATGTTAGTAGAAGCAAAAGCTTGGGATTTGGATCTCTCTTATATCACTCCCT 543
QY 186 AspPheSerLeuMetLeuHisLysArgGluLeuGlnLysArgCysHisSerAsnGlu 205
Db 544 TTTCTTCCCAATCCACCAAAAGCCGACAAAAGCTTCAAAAGATTTCCCTCAATGTT 603
QY 206 MetAspGlyTyr-----LeuAlaTyrIleSerGluGlyLeuGlyAsnLeuTyrAsp 222
Db 604 CTTTCATAACCATCAGACGGCGTTGCTCTACTCTCTGAGGGTTTGGCAAGATGTGGTGAC 663
QY 223 TrpAsnMetValLysLysTyrGlnMetLysAsnGlySerValPheAsnSerProSerAla 242
Db 664 TGGCAAGAGATCAAAATCTTCAATCAAGAGACGGATCATTTTAAAGTCCCTCCCTGCAATC 723
QY 243 ThrAlaAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrLeuAsnSerLeu 262
Db 724 ACTGCTGTGCTCTTCATGACACTCAAAACAAACAGATGCCCTCCACTTCTCACTTCGTG 783
QY 263 LeuAspLysPheGlyAsnAlaValProThrValTyrProHisAspLeuPheIleArgLeu 282
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Qy	283	SerMetValAspThrIleGluuArgLeuGlyIleSerHisPheArgValGluIleLys	302
Db	844	TGGCGCTGCGATACAGTTGAACGCTTGGGAATCGATCGCTATTTCGAAGAAAGAAATCAAA	903
Qy	303	AsnValLeuAspGluThrTyrArgCysTrp---ValGluuArgAspGlu-----	317
Db	904	GAATCTCTGGATTACGTTTATAGTACTCTGGGACGCCGGAAGAGCGGTGGATGGCGCAAGA	963
Qy	318	--GlnIlePheMetAspValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsn	336
Db	964	TGCAATCTCTGATGTCGATGACATGCACTGCCATGGGTCTTAGAATCTCTGAGACTTCAT	1023
Qy	337	GlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu-----	351
Db	1024	GCATACAATGTATCTCTCAGATGTTCTTGAGAAATTCAGAGACGAGAAAGGAGACTCTCTTT	1083
Qy	352	-----LeuAlaLeuLysAspGluTyrAlaAlaLeuGluThrTyr	364
Db	1084	TGCTTTGCCGCTCAACGCCAAATGGTGTGACCGCAATAAT-----CTTAACCTTTTAT	1134
Qy	365	HisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLysGlnIleLeuLysSer	384
Db	1135	AGATGTTTCAAGTATGTTT-----CCGGGAGAAAGATAATATGGAGAA	1179
Qy	385	Ala-----AspPheLeuLysGluIleIleSerThrAsp	395
Db	1180	GCTAAGACCTTCTACTACAAATCATCTCCAAATGCTCTGCCAAAAACAACGCAATTTGAT	1239
Qy	396	SerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAlaLeuLysPheProIle	415
Db	1240	AAGTGGCGGTCTCAAGAGAGATCTCTCTGGAGAGGTGGAGTATGCTATAAAGTATTCCTGG	1299
Qy	416	AsnThrGlyLeuGluuArgIleAsnThrArgArgAsnIleGlnLeuTyrAsnValAspAsn	435
Db	1300	CATAGAAGTATGCCAAGATTCGGAGCGCAAGATTACATAGACCAATTTGGATCAAAATGAT	1359
Qy	436	ThrArgIleLeuLysThrTyrTrpHisSerSerAsnIleSerAsnThrAspTyrLeuArg	455
Db	1360	GTCTGGCTGGGGAAGACTGTGTATAAGATGCTATATGTGACCAACGAAAAATATTTGGAG	1419
Qy	456	LeuAlaValGluuAspPheThrTyrCysGlnSerIleTyrArgGluGluLeuLysGlyLeu	475
Db	1420	CTGCCAAATTTGGACTTCAATATGCTGCAGCGCTTACACCAAAAGGAGACTCAACACAT	1479
Qy	476	GluArgTrpValValGluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThrAla	495
Db	1480	GTCAGCTGGTGAGAGAATCGGGATTCAATGATCTTCACTTCCCGCCACGCGCTGTG	1539
Qy	496	TyrCysTyrPheSerValAlaAlaThrLeuSerSerProGlnLeuSerAspAlaArgIle	515
Db	1540	GAATATGATTTCTCAGTGGCGGTAGTATGTTTGAGCCAGAATTCGCTGCTGTAGAAAT	1599
Qy	516	SerTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhePheAspIleGlyGly	535
Db	1600	GCCATGCCAAGACTTCTGCTCGCAGTATTCTACACGATCTTTACGACACCCACCGGA	1659
Qy	536	ThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAsp	555
Db	1660	TCTCTGATGATCTTAAATTTGTTCTCTGAAGCGGTCCGAAGATGGGATATCTCTGTGCTG	1719
Qy	556	LysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCys	575
Db	1720	GATAGCTTCGGGATAATTCAGTTGAAAGTTTGTCTCTAGCGCTGTACCAACAGTGAAT	1779
Qy	576	TrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGln	595
Db	1780	GGATTTGGAAAAGATGGACTCAAGAACAGGCCGCTGATGTCTGGGCTATCTTCGAAA	1839
Qy	596	ThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyr	615
Db	1840	GTATGGGAGGCTTGCTCGATCTGATATACCAAGAGCCGAATGGTGGGAGCAAGATAT	1899

Qy	616	ValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIle	635
Db	1900	GTCCCGCAATTCACGAATATGTGGAAAAATGCCAAAAGTGTCCATAGCATTTGCGACAGTC	1959
Qy	636	ValLysProAlaIleTyrPheValGlyProLysLeuSerGluGluIleValGluSerSer	655
Db	1960	GTAATAACTCAATCTTTTTCACCTGGAGAAATTAATTCCTCGATTACATATTTTACAGCAAGTA	2019
Qy	656	GluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIle	674
Db	2020	GACCTTCGGTCCAAATTTCTGCATCTTGTCTCTTGTGACTGGACGACTAATCAATGACACC	2079
Qy	675	HisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSer	694
Db	2080	AAGACTTACAGCCCGCAGAGAAACCGTGGTGAATTTGGTTTCCACGCTACAGTG-CTACAT	2138
Qy	695	AsnGlyGluSerGlyLys-ValGluGluGluValValGluMetMetMetMetIleLys	714
Db	2139	GAGGGAATATCCCGATGGTCACAGAGAGAAGCTCTAAGTCATGTTTATGGTATCATCGA	2198
Qy	714	AsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlySerIleValProAr	734
Db	2199	CAACGCACCTGAAGGAATTG---AATTGGGAGTTGGCCAAACCCAGCGAGCAATGCCCCATT	2255
Qy	734	GAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePheTyrAlaAsnAs	754
Db	2256	GTGTGTGAGAAGACTGCTGCTCAACACTGCAGAGGTGATGCAGCTGTTTATATGTACAG	2315
Qy	754	pAspGlyPhe-----ThrGlyAsnThrIleLeuAspThrValLysAspIleIleTyrAs	772
Db	2316	AGATGGCTTTGGTATCTCTGCACAAGAGATGAAGACCATGTGCAGCGGAACCTCTTTTTCGA	2375
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US-10-041-007-34			
; Sequence 34, Application US/10041007			
; Patent No. 6946283			
; GENERAL INFORMATION:			
; APPLICANT: Matsuda, Seiichi P.T.			
; ATTORNEY: Schepmann, Hala G.			
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase			
; FILE REFERENCE: P02081051			
; CURRENT APPLICATION NUMBER: US/10/041,007			
; CURRENT FILING DATE: 2002-01-07			
; PRIOR APPLICATION NUMBER: US 60/259,881			
; PRIOR FILING DATE: 2001-01-05			
; NUMBER OF SEQ ID NOS: 41			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 34			
; LENGTH: 2445			
; TYPE: DNA			
; ORGANISM: Ginkgo biloba			
US-10-041-007-34			
Alignment Scores:			
Pred. No.: 8,25e-112 Length: 2445			
Score: 1075.00 Matches: 261			
Percent Similarity: 52.1% Conservative: 157			
Best Local Similarity: 32.5% Mismatches: 332			
Query Match: 26.1% Indels: 54			
DB: 3 Gaps: 13			
US-10-041-018-383 (1-784) x US-10-041-007-34 (1-2445)			
Qy	10	ProLeuLeuThrLysSerAsnArgProAlaAlaLeuSerAlaIleHisThrAlaSerThr	29
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Qy	30	SerHisGlyGlyGlnThrAsnProThrAsnLeuIleAspThrThrLysGluArgIle	49

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Qy 67 TrpValAlaMetValProSerProAsnSerProLysSerProCysPheProGluCysLeu 86
Db 259 TGGGTGGCAAGAAATTCGATGACGGCTCTGGTGCACCCCAATTTCCCAACAGCTT 318
Qy 87 AsnTrpLeuLeuAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHisThrHis 106
Db 319 CAATGGATTCGAAACAATCAATGCCAGATGGCTCGTGGGGT----- 360
Qy 107 AsnHisAsnHisProLeuLeuLysAspSerSerThrLeuAlaCysIleValAla 126
Db 361 GAGGAGTGCATTTTCTGGCGTATGACAGAGTTTAAACACTCTCGCCTCCCTCACT 420
Qy 127 LeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPheIleGluSer 146
Db 421 CTCAAAATATGGAATAGGCGGACATTCAGTGCAGAAAGGGTTGAGTTTGTGAGAAA 480
Qy 147 AsnLeuAlaSer---AlaThrGluLysSerGlnProSerProIleGlyPheAspIleIle 165
Db 481 CACATGGAAGAAATGAAAGGACGAGCTGACAATCACAGGCGCAAGTGGATTGAGGTG 540
Qy 166 PheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsnLeuSerLysGlnThr 185
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Qy 186 AspPheSerLeuLeuHisLysArgGluLeuGlnLysArgCysHisSerAsnGlu 205
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Qy 337 GlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu----- 351
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Qy 352 -----LeuAlaLeuLysAspGluTyrAlaAlaLeuGluThrTyr 364
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Qy 365 HisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLysGlnIleLeuLysSer 384
Db 1192 AGATGTTTCACAGATGTTT-----CCGGGAGAAAGATAATGGAAGAA 1236

Qy 385 Ala-----AspPheLeuLysGluIleIleSerThrAsp 395
Db 1237 GCTAAGACCTTCACTACAATCATCTCCAAATGCTCTGCCAAACCAACGCAATTTGAT 1296
Qy 396 SerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAlaLeuLysPheProIle 415
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Db 1357 CATAGAAGTATGCCAAGATTGGAGGCAAGAGTTTACATAGCAATTTGGATCAATGAT 1416
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Qy 476 GluArgTrpValValGluAsnLysLeuAspGlnLysPheAlaArgGlnLysThrAla 495
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Qy 496 TyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIle 515
Db 1597 GAATGTATTTCTCAGTGGCGGTAGTATGTTTGGCCAGAAATTCGCTGCTGTAGAAAT 1656
Qy 516 SerTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhePheAspIleGlyGly 535
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Qy 576 TrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGln 595
Db 1837 GGATTTGGAAAGATGAGACTCAAGGAACAGCGCGTGTGCTGGCTATCTTCGAAAA 1896
Qy 596 ThrTrpLeuLeuMetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyr 615
Db 1897 GTATGGGAGGCTTGTCTGCATCGTATCCAAAGAACCGAATGCTCGGACGCAAGATAT 1956
Qy 616 ValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIle 635
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Qy 636 ValLysProAlaIleTyrPheValGlyProLysLeuSerGluLeuValGluSerSer 655
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Qy 675 HisSerPheLysArgGluPheLysGluLysLeuAsnAlaValAlaLeuHisLeuSer 694
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Qy 714 sAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlnSerIleValProAr 734
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QY 734 gAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePheTyrAlaAsnAs 754
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 US-10-041-007-32
 ; Sequence 32, Application US/10041007
 ; Patent No. 6946283
 ; GENERAL INFORMATION:
 ; APPLICANT: Matsuda, Seichi P.T.
 ; APPLICANT: Schepmann, Hala G.
 ; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
 ; FILE REFERENCE: P02081US1
 ; CURRENT APPLICATION NUMBER: US/10/041,007
 ; PRIOR FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: US 60/259,881
 ; PRIOR FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 32
 ; LENGTH: 2622
 ; TYPE: DNA
 ; ORGANISM: Ginkgo biloba
 US-10-041-007-32
 Alignment Scores:
 Pred. No.: 9,31e-112 Length: 2622
 Score: 1075.00 Matches: 261
 Percent Similarity: 52.1% Conservative: 157
 Best Local Similarity: 32.5% Mismatches: 332
 Query Match: 26.1% Indels: 54
 DB: 3 Gaps: 13
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 Db 436 TGGGTGGCAAGAATTCCGTCAATTGACGGCTCTGTGTCACCCCAATTTCCCAACAGCTT 495
 QY 87 AsnTrpLeuIleAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHisThrHis 106
 Db 496 CAATGGATTCTGAACAATCAACTGCCAGATGGCTCGTGGGT----- 537
 QY 107 AsnHisAsnHisProLeuLysAspSerLeuSerSerThrLeuAlaCysIleValAla 126
 Db 538 GAGGAGTCATTTTCTGGCGTATGACAGAGTTTAAACACTCTGCCTGCCCTCCCTCACT 597
 QY 127 LeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPheIleGluSer 146
 Db 598 CTCMAAATATGGAATGAAGGCGACATTAAGTGCAGAAAGGGGTTCAGTTCGTGAGAAA 657
 QY 147 AsnLeuAlaSer---AlaThrGluLysSerGlnProSerProIleGlyPheAspIleIle 165
 Db 1714 GTCAGCTGGTGGAGAGAAATCGGGAATCAATGATCTTACATTCACCCGCCCGCGCTGTG 1773

Db 658 CACATGGAGAATAATGAAGCAGCAAGCTGACAACTCACAGGCCAAGTGGATTCCAGGTCGTG 717
 QY 166 pheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsnLeuLeuSerLysGlnThr 185
 Db 718 TTTCTCTGCAATGTAGATGAAGCAAAAGACTTGGGATTTGGATTCCTCTTATCACCTCCCT 777
 QY 186 AspPheSerLeuMetLeuHisLysArgGluLeuGluGlnLysArgCysHisSerLeuGlu 205
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 QY 206 MetAspGlyTyr-----LeuAlaTyrIleSerGluGlyLeuGlyAsnLeuTyrAsp 222
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 Db 1369 AGATGTTTCAAGTATGTTTT-----CCGGAGAGAAAGATAATGGAAGAA 1413
 QY 385 Ala-----AspPheLeuLysGluIleIleSerThrAsp 395
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 QY 396 SerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAlaLeuLysPheProIle 415
 Db 1474 AAGTGGCTGTCAAGAGGATCTCTCTGAGAGGTGGAGTATGCTATAAGTATCCGTGG 1533
 QY 416 AsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeuTyrAsnValAspAsn 435
 Db 1534 CATAGAGTATGCCAAGATTGGAGGCAAGACTTACATAGCAATTTGATCAATGAT 1593
 QY 436 ThrArgIleLeuLysThrThrTyrHisSerSerAsnIleSerAsnThrAspTyrLeuArg 455
 Db 1594 GTCTGGCTGGGGAAGACTGTGTATAAGATGCTATATGTAGCAACCGAAAAATATTGGAG 1653
 QY 456 LeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGluGluLysGlyLeu 475
 Db 1654 CTGGCCAAATTCGACTTCAATATGTCAGGCTTACACCAAAAGGAGACTCAACACT 1713
 QY 476 GluArgTrpValValGluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThrAla 495
 Db 1714 GTCAGCTGGTGGAGAGAAATCGGGAATCAATGATCTTACATTCACCCGCCCGCGCTGTG 1773

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QY 496 TyxCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIle 515
Db 1774 GAATGTAATTCAGTGGCGGTAGTATGTTGAGCAGAAATCGTGTCTGTAGAAAT 1833
QY 516 SerTrpAlaLysAsnGlyIleLeuThrThrValValAspPhePheAspIleGlyGly 535
Db 1834 GCCTATGCCAAGACTTCTTCCCTCGCAGTATTATCTAGACGATCTTTACGACACCCGGA 1893
QY 536 ThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAsp 555
Db 1894 TCTGTGATGATCTTAATTTGTTCTGGAAGCGTCCGAAGATGGGATATCTCTGTGCTG 1953
QY 556 LysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCys 575
Db 1954 GATAGCGTTCGGGATAATCAGTTGAAAGTTTGTCTCTAGGCTGTACACACAGTGAAT 2013
QY 576 TrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGln 595
Db 2014 GGATTTGGAAAGAGTGAATCAAGGAACAAGCGGTGATGTCTGGGCTATCTTCGAAA 2073
QY 596 ThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyr 615
Db 2074 GTATGGAGGCGTGTCTCGATCGTATACCAAGAACCGCAATGGTGGCAGCAAAAGTAT 2133
QY 616 ValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIle 635
Db 2134 GTCCGACATTCACGCAATATGGAATATGCCAAGTGTCCATAGCATTTGGCAGATC 2193
QY 636 ValIleProAlaIleTyrPheValGlyProLysLeuSerGluGluIleValGluSerSer 655
Db 2194 GTACTAAATCAATCTTTTCACTGGAGAAATTAATCTCTCATTTACATTTTACAGCAAGTA 2253
QY 656 GluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIle 674
Db 2254 GACCTTGGGTCCAAATTTCTGCATCTGTGTCTTTGACTGGCAGCACTAATCAATGACACC 2313
QY 675 HisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSer 694
Db 2314 AAGACTTACAGCGCGGAGAAACCGTGGTGAATGGTTTCCAGCGTACAGTG-CTACAT 2372
QY 695 AsnGlyLysSerGlyLys-ValGluGluGluValValGluMetMetMetMetIleIle 714
Db 2373 GAGGGAATTCGGAGTGACAGAGGAAGTCTTAAGTCATGTTTATGTATCATCGA 2432
QY 714 AsnLysArgGluLeuMetLysLeuIlePheGluGluAsnGlySerIleValProAr 734
Db 2433 CAACGCACTGAAGGAATTG---AATTGGGAGTTGGCCCAACCCAGCAGCAATGCCCAT 2489
QY 734 gAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePheTyrAlaAsnAs 754
Db 2490 GTGTGTGAGAGACTGCTGTCTCAACTGCAAGAGTATGACTGTTTATATGTACAG 2549
QY 754 pAspGlyPhe-----ThrGlyAsnThrIleLeuAspThrValLysAspIleIleTyrAs 772
Db 2550 AGATGGCTTTGGTATCTCTGACAAAGAGATGAAGACCATGTCTCAGCGCACTCTTTTCCA 2609
QY 772 nProLeu 774
Db 2610 TCCTGTG 2616
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RESULT 8

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US-09-398-395A-55
; Sequence 55, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6468772, Joseph P.
; APPLICANT: Starks, Courtney M.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
```

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; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
; US-09-398-395A-55
```

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Alignment Scores:
Pred. No.: 2,89e-110 Length: 2861
Score: 1062.50 Matches: 261
Percent Similarity: 50.6% Conservative: 148
Best Local Similarity: 32.3% Mismatches: 339
Query Match: 25.8% Indels: 61
DB: 3 Gaps: 17
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US-10-041-018-383 (1-784) x US-09-398-395A-55 (1-2861)

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QY 7 IleAlaSerProLeuLeuThrLysSerAsnArgProAlaAlaLeu-----SerAla 23
Db 237 CTTTCTCTCTTACTTGGTGAACGAGAAATTTCTCCAGGATTTTGGAGGATGATCTT 296
QY 24 IleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleIleAsp 43
Db 297 ATCGATTCTTCAACGTCATCTCAAGGTTGCGAGCATCAGACGAGAAGCGT---ATCGAG 353
QY 44 ThrThrLysGluArgIleGlnLysGlnPheLysAsnVal-----GluIleSerVal 60
Db 354 ACATTAAATATCCGAGATTAGAATATGTTTATGTATGGGCTATGGCGAAACGAATCCC 413
QY 61 SerSerTyrAspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerPro 80
Db 414 TCTGCATATGACATCTCTTGGGTAGCAAGGATTTCCAGCAGTTCATGCTCTGCAACACCT 473
QY 81 CysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGly 100
Db 474 CACTTTCTCGAGACGGTTGAAATGGATTTCTCAAAATCAGTTGAAAGATGGGTCTTGGGT 533
QY 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLysAspSerSerSerThr 120
Db 534 -----GAAGGATTTCTTCTTGGCATATGACAGAAATCTAGTCTATAGGCCA 575
QY 121 LeuAlaCysIleValAlaLeuLysAspTrpAsnValGlyGluAspGlnIleAsnLysGly 140
Db 576 CTTGCATGATATTATTACCTTACCCTCTCGCGTACTGGGGAGACACAAGTACAGAAAGGT 635
QY 141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnPro---SerPro 159
Db 636 ATTGAATTTCTCAGGACACAAGCTGGAAAGATGGAAGATGAAGCTGATAGTCTATAGGCCA 695
QY 160 IleGlyPheAspIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsn 179
Db 696 AGTGGATTGAAATAGTATTTCTTCCAAATGCTAAGAAAGCTAAATCTTAGGCTTGGAT 755
QY 180 LeuLeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGluGlnLys 199
Db 756 CTGCCTTACGATTTGGCCATTTCTTGAAACAAATCATCGAAAGCGGGAGGCTAGCTTAA 815
QY 200 ArgCysHisSerAsn-----GluMetAspGlyTyrLeuAlaTyrIleSerGluGly 216
Db 816 AGGATCCCACTGATGTTCTCTATGCCCTTCCAAACCAACGTTATGTATTCTTTGGAAGGT 875
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Qy	217	LeuGlyAsnLeuTyrAspThrAsnMetValIysLysTyrGlnMetLysAsnGlySerVal	236
Db	876	TTCAAGAAATAGTAGATCGCAGAAATATGAAATCTCAATCCAAGGATGGATCATTT	935
Qy	237	PheAsnSerProSerAlaThrAlaAlaAlaPheIleAsnHisGlnAsnProGlyCysLeu	256
Db	936	CTCAGCTCTCCGGCATCTACAGCGCTGTATTATCATGGTACAGGAAACAATAAGTGTCTG	995
Qy	257	AsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrProHis	276
Db	996	GATTTCTTGAACTTGTCTTGAAGAAATTCGAAACCATTGCTGTCTACTATCCGCTT	1055
Qy	277	AspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHisHis	296
Db	1056	GATCTATTTGAAACGTTTGTGGCGGTTGTATACAGTTGAGCGGCTAGGTATCGATCGTCAT	1115
Qy	297	PheArgValGluIleLysAsnValLeuAspGluThrTyrArgCysTrrpValGluArgAsp	316
Db	1116	TTCAAGAGGAGATCAAGGAAGCATTTGGATTATGTTTACAGCCATTGGGACGAAAGAGGC	1175
Qy	317	-----GluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg	331
Db	1176	ATTGGATGGCGGAGAGAGATCTCTGTTCTTGATATTGATGATACAGCATGGCGCTTCGA	1235
Qy	332	LeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu	351
Db	1236	ATCTTGAGATTACATGATACAATGATCTCTCAGATGTTTAAAAACATTTAGAGATGAG	1295
Qy	352	LeuAlaLeuLysAspGluTyrAlaAla-----	360
Db	1296	-----AATGGGAGAGTTCTTTTGTCTTCTGGTCAAAACACAGAGAGGATTACAGAC	1346
Qy	361	--LeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLys	379
Db	1347	ATGTTAAACGTCAATCGTTGTTACATGTTTCAIT-----CCGGAGAA	1391
Qy	380	GlnIleLeuLysSerAla-----AspPheLeuLysGlu	390
Db	1392	ACGATCATGGAGAAGCAAAACTCTGTACCGAAGGTTATCTGAGGAATGCTCTGGAAAT	1451
Qy	391	IleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla	410
Db	1452	GTGGATCCCTTTGACAAATGGGCTTTTAAAAAGAAATATTCGGGAGAGGTAGAGTATGCA	1511
Qy	411	LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgAsnIleGlnLeu	430
Db	1512	CTCAATATCCCTGGCATAGATATGCCAAGGTTGGAGGCTAGAAGCTATATTGAAAC	1571
Qy	431	TyrAsnValAspAsnThrArgIleLeuLysThrThrTyrHisSerSerAsnIleSerAsn	450
Db	1572	TATGGCCAGATGATGTGCTTGGAAAACTGTATATATGATGCCATACATTTCGAAT	1631
Qy	451	ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu	470
Db	1632	GAATAAGTATTAGAACTTAGCGAAACTGGACTTCAATAAGGTGCGAGTCTATACACCAACA	1691
Qy	471	GluLeuLysGlyLeuGluArgTrrpValValGluAsnLysLeuAspGlnLeuLysPheAla	490
Db	1692	GAGCTTCAAGATCTTCGAAGGTGGTGAATCATCCGGTTTCACGGATCTGAATTTCACT	1751
Qy	491	ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu	510
Db	1752	CGTGAGCGGTGACGGAATATATTTCTACCGGCATCTCTTATCTTTGAGCCGAGTTT	1811
Qy	511	SerAspAlaArgIleSerTrrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhe	530
Db	1812	TCTAAGTCGACAGAGGTTTATACAAAACCTTCCAATTTCACTGTTATTTTAGATGATCTT	1871
Qy	531	PheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrrp	550
Db	1872	TATGACGCCCATGATCTTTAGAGATCTTAAAGTTGTTTCAAGATCAGTCAAAAGATGG	1931
Qy	551	AsnValAspValAspLysAspCysSerGluHisValArgIleLeuPheLeuAlaLeu	570

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RESULT 9
US-09-887-586A-55
; Sequence 55, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6495354I, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ IDS NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-887-586A-55

Alignment Scores:
Pred. No.: 2,896-110 Length: 2861
Score: 1062.50 Matches: 261
Percent Similarity: 50.6% Conservative: 148
Best Local Similarity: 32.3% Mismatches: 339
Query Match: 25.8% Indels: 61
DB: 3 Gaps: 17

US-10-041-018-383 (1-784) x US-09-887-586A-55 (1-2861)

QY 7 IleAlaSerProLeuLeuThrLysSerAsnArgProAlaAlaLeu-----SerAla 23
DB 237 CTTTCCTCTTCTCATTTGGTGAACGAGAAATTCCTCCAGGATTTTGGAAAGGATGCTT 296
QY 24 IleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleAsp 43
DB 297 ATCGATCTCTAAGCTCATCTCACAGGTTGCAGCATCACAGAGAGCGT---ATCGAG 353
QY 44 ThrLysGluArgIleGlnLysGlnPheLysAsnVal-----GluIleSerVal 60
DB 354 ACATTAATATCCGAGATTAAGAATATGTTTAGATGTATGGCTATGGCGAAACGAATCCC 413
QY 61 SerSerThrAspThrAlaTTPValAlaMetValProSerProAsnSerProLysSerPro 80
DB 414 TCTGCATATACACATGCTGGTAGCAAGATTCCAGCAGTTGATGGCTCTGCAACCCCT 473
QY 81 CysPheProGluCysLeuAsnTTPLeuIleAsnAsnGlnLeuAsnAspGlySerTPGly 100
DB 474 CACTTCTCGAGAGCGTTGAATGATGATCTTCAAAATCAGTTGAAGATGGGTCTTGGGT 533
QY 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLysAspSerLysSerThr 120
DB 534 -----GAAGGATTTCTACTTCTTGGCATATGACAGAAATCTGGCTACA 575
QY 121 LeuAlaCysIleValAlaLeuLysArgTTPAsnValGlyGluAspGlnIleAsnLysGly 140
DB 576 CTTGCGATGATTATATACCTTACCTCTGGCGTACTGGGAGACACAAAGTACAGAAAGT 635
QY 141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrLysSerGlnPro---SerPro 159
DB 636 ATTGAATCTTCAGGACACAAAGCTGGAAAGATGGAAGATGAAGCTGATGATAGGCCA 695
QY 160 IleGlyPheAspIleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsn 179
DB 696 AGTGGATTGCAATAGTATTTCTCGCAATGCTAAAGGAAGCTAAATCTTTAGGCTTGGAT 755
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DB 756 CTGCCTTACGATTTGCCATTTCTCTGAACAAATCATCGAAAGCGGGAGGCTAAGCTTTAA 815
QY 200 ArgCysHisSerAsn-----GluMetAspGlyTyrLeuAlaTyrIleSerGluGly 216
DB 816 AGGATTTCCCACTGATGTTCTATGCTTCCCAACAAAGCTTATGTTATTTTGGAAAGGT 875
QY 217 LeuGlyAsnLeuTyrAspTTPAsnMetValLysLysTyrGlnMetLysAsnGlySerVal 236
DB 876 TTACAGAATAATAGTAGACTGCGAGAAAATAATGAACTTCAATCCAGGATGATCATTT 935
QY 237 PheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeu 256
DB 936 CTCAGCTCTCCGGCATCTACAGCGGCTGTATTCATGCGTACAGGAGCAAAAAGTGTCTG 995
QY 257 AsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrProHis 276
DB 996 GATTTCCTTGAACCTTGTCTTGAAGAAATTCGGAACCATGTCCTTCTCATATCCGCTT 1055
QY 277 AspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHis 296
DB 1055 -----

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1056 GATCTATTTGAACGCTTTGTGGCGGTTGATACAGTTGAGCGGCTAGGTATCGATCGTCAT 1115
QY 297 PheArgValGluIleLysAsnValLeuAspGluThrTyrArgCysTTPValGluArgAsp 316
DB 1116 TTCAAAGAGGAGATCAAGGAGCATTGGATTATGTTTACAGCCATTGGGAGCAAGAGGC 1175
QY 317 -----GluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg 331
DB 1176 ATTGGATGGCGAGAGAGAAATCTGTTCTGATATTGATGATACAGCCATGGGCTTCGA 1235
QY 332 LeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu 351
DB 1236 ATCTTGAGATTACATGATCAATGATCTCAGATGTTTAAAAAACAATTAGAGTAGAG 1295
QY 352 LeuAlaLeuLysAspGluTyrAlaAla----- 360
DB 1296 -----AATGGGAGTTCTTTTCTGCTTCTGGTCAACACAGAGAGAGTTACAGAC 1346
QY 361 ---LeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLys 379
DB 1347 ATGTTAAACGTCAATCGTTGTTTCCATGTTTCAATTT-----CCGGGAGAA 1391
QY 380 GlnIleLeuLysSerAla-----AspPheLeuLysGlu 390
DB 1392 ACGATCATGGAAGAACAAACTCTGTACCGAAAGGTATCTGAGGAATGCTCTGGAATA 1451
QY 391 IleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
DB 1452 GTGGATGCTTTCACAAATGCGGCTTTTAAAGAAATATTCGGGAGAGGTAGATATGCA 1511
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DB 1572 TATGGCCAGATGATGTGTGGCTTGGAAAACTGTATATATGATGATGATGATGATGAT 1631
QY 451 ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu 470
DB 1632 GAAAGATATTAGAACTAGCGAAACTGGAATCTCAATAGGTGACGTCTATACCAACA 1691
QY 471 GluLeuLysGlyLeuGluArgTTPValValGluAsnLysLeuAspGlnLeuLysPheAla 490
DB 1692 GAGCTTCAAGATCTTCGAAGTGTGGAAATCATCCGGTTTCAGGATCTGAATTTCACT 1751
QY 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
DB 1752 CGTGAGCGTGTGACGGAATATATTTCTCACCGGCATCTTTATCTTTGAGCCGAGTTT 1811
QY 511 SerAspAlaArgIleSerTTPAlaLysAsnGlyIleLeuThrThrValValAspAspPhe 530
DB 1812 TCTAAGTGCAGAGGTTTATACAAAACTTCCAAATTTCACTGTTATTTAGATGATCTT 1871
QY 531 PheAspIleGlyGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTyr 550
DB 1872 TATGACGCCCATGATCTTTAGACGATCTTAAGTTGTTGCAGAAATCAGTCAAAAGATGG 1931
QY 551 AsnValAspValAspLysAspCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
DB 1932 GATCTATCACTA---GTGGACCAATGCCCAAAATGAAATATGTTTGTGGTTTC 1988
QY 571 LysAspAlaIleCysTTPIleGlyAspGluAlaPheLysTTPGlnAlaAspValThr 590
DB 1989 TACAATATCTTTAATGATATAGCAAAAGAGGACGTGAGAGGCAAGGCGGATGCTCTA 2048
QY 591 SerHisValIleGlnThrTTPLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTyr 610
DB 2049 GGTCTACATCAATGTTTGGAAAGTCCCACTTGAAGCTTACACGAAAGAGCAGATGG 2108
QY 611 ThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPhe 630
DB 2109 TCTGAAGCTAAATATGTGCCATCTTCAATGAATACATAGAGATGCGAGTGTCTCAATA 2168

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QY 631 AlaLeuGlyProIleValIysProAlaIleTyrPheValGlyProIysLeuSerGluGlu 650
 DB 2169 GCAATTTGGGAACATCGTCTTCATTATGCTCTTTTCACTGGGGAGGTTCTTACAGATGAA 2228
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 QY 729 GlySerIleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsn 748
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 DB 2517 CTCCTTTATATCAAGGGATGGTTTGACACTATCACATGATATGGAATTAAGAGCAT 2576
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 DB 2577 GTCAAAATTTGCCCTCTTCCAAACGAGTT 2603

RESULT 10

US-09-895-752-55
 ; Sequence 55, Application US/09895752
 ; Patent No. 6559297
 ; GENERAL INFORMATION:
 ; APPLICANT: Chappell, Joseph
 ; APPLICANT: No. 65592971, Joseph P.
 ; APPLICANT: Starks, Courtney M.
 ; APPLICANT: Manna, Kathleen R.
 ; TITLE OF INVENTION: SYNTHASES
 ; FILE REFERENCE: 07678-025001
 ; CURRENT APPLICATION NUMBER: US/09/895,752
 ; CURRENT FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: 09/398,395
 ; PRIOR FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: 60/100,993
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/130,628
 ; PRIOR FILING DATE: 1999-04-22
 ; PRIOR APPLICATION NUMBER: 60/150,262
 ; PRIOR FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 55
 ; LENGTH: 2861
 ; TYPE: DNA
 ; ORGANISM: Abies grandis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (3)...(2606)
 ; OTHER INFORMATION: abietadiene synthase
 US-09-895-752-55

Alignment Scores:
 Pred. No.: 2,89e-110 Length: 2861
 Score: 1062.50 Matches: 261
 Percent Similarity: 50.6% Conservative: 148
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 Query Match: 25.8% Indels: 61
 DB: 3 Gaps: 17

US-10-041-018-383 (1-784) x US-09-895-752-55 (1-2861)
 QY 7 IleAlaSerProLeuLeuThrLysSerAsnArgProAlaAlaLeu-----SerAla 23
 DB 237 CTTTCTTCTTACATTTGGTGAACAGAAATTTCTCCAGAGATTTTGGGAAGATGATCTT 296
 QY 24 IleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleLeuAsp 43
 DB 297 ATCGAATTTCTTAACGTCTCATCTCAAGAGTTGCGCATCAGACGAGAAGCGT---ATCGAG 353
 QY 44 ThrThrLysGluArgIleGlnLysGlnPheLysAsnVal-----GluIleSerVal 60
 DB 354 ACATTAAATATCCGAGATTAAAGATATGTTAGATGATGGGTATGGCGAAGCAATATCCC 413
 QY 61 SerSerTyrAspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerPro 80
 DB 414 TCTGCATATGACACTGCTTGGGTAGCAAGGATTCAGCAGAGTTTGGGTCTCTGACAAACCT 473
 QY 81 CysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGly 100
 DB 474 CACTTCTCTGACACGCTTGAATGAGATTCTTCAAAATCAGTTGAAAGATGGGTCTTGGGT 533
 QY 101 LeuValAsnHisThrHisAsnHisProLeuLeuLysAspSerLeuSerSerThr 120
 DB 534 -----GAGGATTCTACTTCTTGGCATATGACAGAATATCTGGGTACA 575
 QY 121 LeuAlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGly 140
 DB 576 CTTGCATGATTTATTACCTTACCCTTGGCGTACTGGGGAGACACAAGTACAGAAAGGT 635
 QY 141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnPro---SerPro 159
 DB 636 ATTTGAATTTCTTCAGGACACAAGCTCGAAAGATGGAAGATGAAGCTGATAGTCATAGGCCA 695
 QY 160 IleGlyPheAspIleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsn 179
 DB 696 AGTGATTTGAAATAGTATTTCTGCAATGCTTAAGGAAGCTTAAATCTTTAGCTTGGAT 755
 QY 180 LeuLeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGluLys 199
 DB 756 CTGCTTACGATTTGCCATTTCTCGAAACAAATCATGAAAGCGGAGCTAAGCTTAAA 815
 QY 200 ArgCysHisSerAsn-----GluMetAspGlyTyrLeuAlaTyrIleSerGluGly 216
 DB 816 AGGATTTCCACATGATGTTCTCTATGCCCTTCCAAACACGTTATTTCTTTTGAAGGT 875
 QY 217 LeuGlyAsnLeuTyrAspTrpAsnMetValLysLysTyrGlnMetLysAsnGlySerVal 236
 DB 876 TTACAAGAAATAGTAGACTGGCAGAAATAATGAACCTTCAATCCAGGATGGATCATTT 935
 QY 237 PheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeu 256
 DB 936 CTCAGCTCTCCGGCATCTACAGCGGCTGATTTATGTCGCTACAGGGAACAAAAGTCTTG 995
 QY 257 AsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrProHis 276
 DB 996 GATTTCTTGAACCTTTGCTTGAAGAAATTCGAAACCATGTCCTTGTGCATATCCGCTT 1055
 QY 277 AspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHisHis 296
 DB 1056 GATCTATTGAAACGTTTGTGGCGGTTGTATACAGTTGAGCGGCTAGTATCGATCGTCAT 1115
 QY 297 PheArgValGluIleLysAsnValLeuAspGluThrTyrArgCysTrpValGluArgAsp 316
 DB 1116 TTCAAAGAGGAGATCAAGGAGCATTTGGATTATGTTTACAGCCATTTGGGACGAAAGAGGC 1175
 QY 317 -----GluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg 331
 DB 1176 ATTGGATGGCGAGAGAGAATCTGTTCTGTATATTGATGATACAGCCATGGGCTTCGA 1235
 QY 332 LeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu 351
 DB :::::::::::::::::::: ||||| ||||| ::::

Db 1236 ATCTTGAGATTACATGATCAATGTATCTCAGATGTTTTTAAAAACATTTAGAGATGAG 1295
Qy 352 LeuAlaLeuLysAspGluTyrAlaAla----- 360
Db 1296 -----AATGGGAGATTCTTTTGGTCTTGGGTCAAAACACAGAGAGAGTTACAGAC 1346
Qy 361 ---LeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLys 379
Db 1347 ATGTTAAACGTCATCGTGTTCACATGTTTCATTT-----CCGGGAGAA 1391
Qy 380 GlnIleLeuLysSerAla-----AppheLeuLysGlu 390
Db 1392 ACGATCATGGAAGCAAAACCTCTGTACCAAGGTATCTGAGGATGCTCTGGAAAT 1451
Qy 391 IleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
Db 1452 GTGATGCCCTTGACAAATGGGCTTTTAAAGAAATATTCGGGAGAGGTAGATGCA 1511
Qy 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
Db 1512 CTCATATCCCTGGCATAGATGATGCCAAGGTGGAGGCTAGACGCTATATTGAAAC 1571
Qy 431 TyrAsnValAspAsnThrArgIleLeuLysThrThrTyrHisSerSerAsnIleSerAsn 450
Db 1572 TATGGGCCAGATGATGTGGCTTGGAATAAACTGTATATATGATGCCATACATTTGCAAT 1631
Qy 451 ThrAspTyrLeuArgIleAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu 470
Db 1632 GAAAGATATTAGAACTAGCGAAACCTGGACTTCAATAAGGTGCGAGTCTATACCAACA 1691
Qy 471 GluLeuLysGlyLeuGluAspTyrValValGluAsnLysLeuAspGlnLeuLysPheAla 490
Db 1692 GAGCTTCAAGATCTTGAAGGTGGTGAATATCATCCGGTTCCAGGATCTGAATTCAC 1751
Qy 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
Db 1752 CGTGAGCGTGTGCGGAAATATATTCTCACCGGCATCCTTTATCTTTTGAGCCGAGTTT 1811
Qy 511 SerAspAlaArgIleSerTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhe 530
Db 1812 TCTAAGTGCAGAGAGGTTTATACAAAACCTTCCAATTTCACTGTTATTTAGATGATCTT 1871
Qy 531 PheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTyr 550
Db 1872 TATGACCCCATGATCTTTAGAGATCTTAAGTTGTTTCAGAGATCAGTCAAAAGATGG 1931
Qy 551 AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
Db 1932 GATCTATCACTA--GTGGACCAATGCCACAACAAATGAAATATGTTTGTGGGTTTC 1988
Qy 571 LysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThr 590
Db 1989 TACAATATCTTTAATGATATAGCAAAAGAGAGCGTGTGAGAGCAAGCGCGATGTGCTA 2048
Qy 591 SerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTyr 610
Db 2049 GGCATACATCAAAATGTTTGGAAAGTCCAACTTGAAGCTTACAGCAAAAGAGCAAGTGG 2108
Qy 611 ThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPhe 630
Db 2109 TCTGAAGCTAAATATGTGCCATCTTCAATGAATACATACAGAAATGCGAGTGTCAATA 2168
Qy 631 AlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLysLeuSerGluGlu 650
Db 2169 GCATTGGGAACAGTCGTCTCTCATTAAGTGTCTTTTCACTCGGGAGGTTCTTACAGATGAA 2228
Qy 651 IleValGluSerSerGluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArg 669
Db 2229 GTACTCTCCAAATATGATCGCAATCTAGATTTCTTCAATCATGGGCTTAACAGGCGT 2288
Qy 670 LeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaVal 689
Db 2289 TTGGTGNATGACCAAAACCTTATCAGGAGAGAGGTCNAGGTGAGGTG--GCTTCT 2345

Qy 690 AlaLeuHisLeuSerAsnGlyGluSerGlyLysVal---GluGluGluValValGluGlu 708
Db 2346 GCCATACATGTTATATGAAGGACCATCTTAATCTCTGAAGAAAGAGCTCTACACAT 2405
Qy 709 MetMetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsn 728
Db 2406 GTCTATAGTGTCTATGGAATAATGCCCTCGAAGAGTTGAATAGG-----GAGTTTGTG 2456
Qy 729 GlySerIleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsn 748
Db 2457 AATAACAAATATACCGGATATTTACAAAAGACTGCTTTTGAACCTGCAAGAATAATCA 2516
Qy 749 PhePheTyrAlaAsnAspAspGlyPheThr-----GlyAsnThrIleLeuAspThr 765
Db 2517 CTCTTTATATGCAAGGGATGTTGACACTATCATCATGATATGGAANTTAAGAGCAT 2576
Qy 766 ValLysAspIleIleTyrAsnProLeu 774
Db 2577 GTCAAAATTCCTCTTCCAACCATGTT 2603

RESULT 11

US-09-903-012B-55
; Sequence 55, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-903-012B-55

Alignment Scores:
Pred. No.: 2,89e-110 Length: 2861
Score: 1062.50 Matches: 261
Percent Similarity: 50.6% Conservative: 148
Best Local Similarity: 32.3% Mismatches: 339
Query Match: 25.8% Indels: 61
DB: 3 Gaps: 17

US-10-041-018-383 (1-784) x US-09-903-012B-55 (1-2861)

Qy 7 IleAlaSerProLeuLeuThrLysSerAsnArgProAlaAlaLeu-----SerAla 23
Db 237 CTTTCTCTTCTCATTTGTTGAACGAGAAATTTCTCCAGGATTTTGGAGGATGATCTT 296
Qy 24 IleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleAsp 43
Db 297 ATCGATTCTTCAACGTCATCTCACAGGTTGCGAGCATCAGACGAGAACGCT---ATCG 353
Qy 44 ThrThrLysGluArgIleGlnLysGlnPheLysAsnVal-----GluIleSerVal 60
Db 354 ACATTAATATCCGAGATTAGAATATGTTTAGATGTTGGCTATGCGCAACGAATCCC 413


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QY 61 SerSerTyAspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerPro 80
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
414 TCTGCATATGACATGCTTGGGTAGCAAGATTCACGACGATTCAGCGCTCTGCACACCC 473
QY 81 CysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGly 100
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
474 CACTTTCCTGACGCGTTCGAATGGATCTTCAAAATCAGTTGAAAGATGGGTCTTGGGGT 533
QY 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLeuLysSerSerSerThr 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
534 -----GAAGATCTCTACTCTTGGCATATGACAGATATCGGTAC 575
QY 121 LeuAlaCysIleValAlaLeuLysArgTrpAsnValGluAspGlnIleAsnLysGly 140
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
576 CTTGCATGTATTATTACCTTACCCTCTGGCTACTGGGAGACACAAAGTACAGAAAGGT 635
QY 141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnPro---SerPro 159
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
636 ATTGAATCTTCAGGACACCAAGCTGGAAGATGGAGATGAAGCTGATAGTCATAGGCCA 695
QY 160 IleGlyPheAspIleIlePheProGlyLeuLeuGluTyAlaLysAsnLeuAspIleAsn 179
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
696 ACTGGATTGAATAGTATTCTGCAATGCTAAAGAAAGCTAAATCTTAGCGCTTGGAT 755
QY 180 LeuLeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGlnLys 199
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
756 CTGCCTTACGATTGCCATTCTCGAAACAAATCATCGAAAGCGGAGCTAAGCTTAA 815
QY 200 ArgCysHisSerAsn-----GluMetAspGlyTyAlaAlaTyIleSerGluGly 216
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
816 AGGATTCACCTGATGTTCTCTATGCCCTTCCAAACAAAGCTTATTGTTCTTTGGAAGT 875
QY 217 LeuGlyAsnLeuTyAspTrpAsnMetValLysLysTyAlaMetLysAsnGlySerVal 236
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
876 TTACAAGAAATAGTAGACTGGCAGAAATAAATAAATCAATCCAGAGTGCATCATTT 935
QY 237 PheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeu 256
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
936 CTCAGCTCTCCGGCATCTACAGCGCTGTATTTCATCGGTACAGGGAACAAAAGTGTG 995
QY 257 AsnTyLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyProHis 276
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
996 GATTTCTTGAACTTGTCTTGAGAAATTCGGAACCATGTGCTGTGCATCTATCGCTT 1055
QY 277 AspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHis 296
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1056 GATCTATTGAACGTTTGGCGGTTGTATACAGTTGACGCTAGGTATCGATCGTCAT 1115
QY 297 PheArgValGluIleLysAsnValLeuAspGluThrTyArgCysTrpValGluArgAsp 316
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1116 TTCAAAGAGGAGATCAAGGAAGCATTTGGATTATGTTTACAGCCATTTGGACGAAAGAG 1175
QY 317 -----GluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg 331
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1176 ATTGGATGGCGAGAGAGAATCCTGTTCTGTATATTGATGATACAGCCATGGCGCTTGA 1235
QY 332 LeuLeuArgIleAsnGlyTyArgValSerProAspProLeuAlaGluIleThrAsnGlu 351
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1236 ATCTTGAGATTACATGATGATCAATGTATCTCAGATGTTTAAAAACATTTAGAGATGAG 1295
QY 352 LeuAlaLeuLysAspGluTyAlaAla----- 360
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1296 -----AATGGGAGGTCTTTTGTCTTCTTGGGTCAAAACACAGAGGAGGTACAGAC 1346
QY 361 ---LeuGluThrTyHisAlaSerHisIleLeuTyArgGlnGluAspLeuSerSerGlyLys 379
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1347 ATGTTAAACGTCAATCGTTGTTTACATGTTTCATTT-----CCGGAGAA 1391
QY 380 GlnIleLeuLysSerAla-----AspPheLeuLysGlu 390
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1392 ACGATCATGGAAGAGCAAACTCTGTACCGAAAGGTATCTGAGGAATGCTCTGGAAAT 1451
QY 749 PhePheTyAlaAsnAspAspGlyPheThr-----GlyAsnThrIleLeuAspThr 765
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QY 391 IleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1452 GTGGATGCTTTCACAAATATGGCTTTTAAAAAGAAATATTCGGGGAGAGGTAGATATGCA 1511
QY 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1512 CTCAAATATTCCTGCATAGAGTATGCCAAGGTGGAGGCTGAGAGCTATATTGAAAC 1571
QY 431 TyrAsnValAspAsnThrArgIleLeuLysThrTyHisSerSerAsnIleSerAsn 450
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1572 TATGGCCAGATGATGTGGCTTCGAAAACCTGTATATATGATGATCCATATTCGAAT 1631
QY 451 ThrAspTyLeuArgLeuAlaValGluAspPheTyThrCysGlnSerIleTyArgGlu 470
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1632 GAAAAAGTATTAGAACTAGCGAAACTGGCACTTCAATAAGGTGAGCTCTATACCAACAA 1691
QY 471 GluLeuLysGlyLeuGluArgTrpValValGluAsnLysLeuAspGlnLysPheAla 490
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1692 GAGCTTCAAGATCTTCGAAGGTGGTGGAAATCATCCGGTTTCAGGATCTGAATTTCACT 1751
QY 491 ArgGlnLysThrAlaTyCysTyPheSerValAlaAlaThrLeuSerSerProGluLeu 510
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1752 CGTAGCGGTGACGGAATAATATTTCTCAGCGCATCCCTTTATCTTTCAGCCCGAGTTT 1811
QY 511 SerAspAlaArgIleSerTrpAlaLysAsnGlyIleLeuThrValValAspAspPhe 530
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1812 TCTAAGTGCAGAGAGGTTTATACAAAACTTCCAATTTCACTGTTATTTAGATGATCTT 1871
QY 531 PheAspIleGlyGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrp 550
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1872 TATGACGCCATGATCTTTAGCAGATCTTAAGTGTTCACAGATCATGTCAAAAGATGG 1931
QY 551 AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1932 GATCTATCACTA--GTGGACCAATGCCACAAACAAATGAAATATGTTTGTGGGTTTC 1988
QY 571 LysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThr 590
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1989 TACAATACTTTTAAATGATATAGCAAAAGAGACGCTGAGAGCAAGGGCGCATGTGCTA 2048
QY 591 SerHisValIleGlnThrTrpLeuGluMetAsnSerMetLeuArgGluAlaIleTrp 610
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2049 GGTCAATTCAAAATGTTTGGAAAGTCCAACTTGAGGCTTACACGAAAGACAGATGG 2108
QY 611 ThrArgAspAlaTyValProThrLeuAsnGluTyMetGluAsnAlaTyValSerPhe 630
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2109 TCTGAAGCTAAATATGTCCATCTTCAATGAATACATAGAGAATCGAGTGTGCTCAATA 2168
QY 631 AlaLeuGlyProIleValLysProAlaIleTyPheValGlyProLysLeuSerGluGlu 650
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2169 GCATTTGGGAACAGTCGTTCTCATTTAGTCTCTTTTCACTGGGGAGGTTCTTACAGATGA 2228
QY 651 IleValGluSerSerGluTyHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArg 669
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2229 GTACTCTCCAAATGTATGCGCAATCTAGATTTCTTCAACTCATGGGCTTAACAGGCGGT 2288
QY 670 LeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaVal 689
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2289 TTGGTGAATGACACCAAACTTATCAGGCAGAGAGGCTCAAGGTGAGGTG--GCTTCT 2345
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2346 GCCATACAATGTATATGAAGGACCATCTCTAAATCTCTGGAAGAGAACTCTTACAACAT 2405
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2406 GTCTATAGTGTCTATGAAAAATGCCCTCGAAGAGTGAATAGG-----GAGTTTGTG 2456
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Db 2517 CTCTTTATATGCAAGGGATGTTTGACACTATCATCATGATATGGAATAATAAGAGCAT 2576
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Db 2577 GTCAAAATTTGCCTCTTCCAACCAAGTT 2603

RESULT 12
US-09-900-797-55
; Sequence 55: Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCES: 07678-025001
; CURRENT FILING DATE: 2001-07-06
; PRIOR FILING DATE: US/09/900,797
; PRIOR FILING DATE: US/09/398,395
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-900-797-55

Alignment Scores:
Pred. No.: 2,89e-110 Length: 2861
Score: 1062.50 Matches: 261
Percent Similarity: 50.6% Conservative: 148
Best Local Similarity: 32.3% Mismatches: 339
Query Match: 25.8% Indels: 61
DB: 3 Gaps: 17

US-10-041-018-383 (1-784) x US-09-900-797-55 (1-2861)
Qy 7 IleAlaSerProLeuLeuThrLysSerAsnArgProAlaAlaLeu-----SerAla 23
Db 237 CTTTCTTCTACATGTTGTAACCGAGAAATTTCTCCAGGATTTTGGAGGATGATCTT 296
Qy 24 IleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleAsp 43
Db 297 ATCGATTCTCAACGTCATCTCACAGGTTGCAGCATCAGACGAGAGCGT---ATCGAG 353
Qy 44 ThrThrLysGluArgIleGlnLysGlnPheLysAsnVal-----GluIleSerVal 60
Db 354 ACATTAATATCCGAGATTAAGAAATATGTTAGATGATGCGGCTATGCGCGAAACGAATCCC 413
Qy 61 SerSerTyraAspThrAlaTpvAlaMetValProSerProAsnSerProLysSerPro 80
Db 414 TCTGCATATGACATCTCTTGGTAGCAAGGATTCAGGATTCAGGCTGATGCTCTGCAACCCCT 473
Qy 81 CysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGly 100
Db 474 CACTTTCTCGAGCGGTTGAATGGAATCTTCAAAATCAGTTGAAGATGGGTCTTGGGGT 533
Qy 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLysAspSerLeuSerThr 120
Db 534 -----GAAGGATTCTACTTCTTGGCATATGACAGAAATACTGGCTACA 575
Qy 121 LeuAlaCysIleValAlaLeuLysArgTpvAsnValGlyGluAspGlnIleAsnLysGly 140
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Db 576 CTTGCAATGATTATTATCCCTTACCCCTCTGCGCTACTGGGAGACACAAGTACAGAAAGGT 635
Qy 141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnPro---SerPro 159
Db 636 ATTGAATTTCTTCAGGACACAAAGCTGGAAGATGGAAGATGAAGCTGATGATCATAGGCCA 695
Qy 160 IleGlyPheAspIleIlePheProGlyLeuLeuGluTyraAlaLysAsnLeuAspIleAsn 179
Db 696 AGTGGATTTGAATAGTATTCTCTCAATGCTAAAGGAAGCTAAATCTTAGGCTTGAT 755
Qy 180 LeuLeuSerLysGlnThrAspPheSerLeuMetHisLysArgGluLeuGlnLys 199
Db 756 CTGCCTTACGATTTCCTGAAACAAATCATCGAAAGCGGAGGCTAAGCTTAA 815
Qy 200 ArgCysHisSerAsn-----GluMetAspGlyTyraLeuAlaTyrlleSerGluGly 216
Db 816 AGGATTTCCCACTGATGTTCTATATGCCCTTCCAAACAGCTTATTTGTTATCTTTGGAAGGT 875
Qy 217 LeuGlyAsnLeuTyraAspTrpAsnMetValLysLysTyraGlnMetLysAsnGlySerVal 236
Db 876 TTACAAGAAATAGTAGACTGGCAGAAATAATGAACTTCAATCCAAGGATGATCATTT 935
Qy 237 PheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeu 256
Db 936 CTCAGCTCTCCGGCATCTACAGCGGTGTTATTCATCGGTACAGGACAAAGAGTGTG 995
Qy 257 AsnTyraLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyraProHis 276
Db 996 GATTTCTTGAACCTTTCTTGAAGAAATTCGGAACCATGTGCTTGTCTCATATCCGCTT 1055
Qy 277 AspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHis 296
Db 1056 GATCTATTGAACTTTTGGCGGTTGATACAGTTGAGCGGTAGGTATCGATCGTCAT 1115
Qy 297 PheArgValGluIleLysAsnValLeuAspGluThrTyraArgCysTrpValGluArgAsp 316
Db 1116 TTCAAAGAGGAGATCAAGGAAGCATTTGGATTATGTTTACAGCCATTTGGGACGAAGAGGC 1175
Qy 317 -----GluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg 331
Db 1176 ATTGGATGGCGGAGAGAGAAATCTGTTCCTGATATTGATGATACAGCATGGGCTTCGA 1235
Qy 332 LeuLeuArgIleAsnGlyTyraValSerProAspProLeuAlaGluIleThrAsnGlu 351
Db 1236 ATCTTGAGATTACATGATACATGATCTCTCAGATGTTTAAACACATTTAGAGATGAG 1295
Qy 352 LeuAlaLeuLysAspGluTyraAlaAla----- 360
Db 1296 -----AATGGGAGTTCTTTTCTCTTGGTCAAAACACAGAGAGGATTACAGAC 1346
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Db 1347 ATGTTAAACGTCAATCGTTGTTCCATGTTTCAATTT-----CCGGAGAA 1391
Qy 380 GlnIleLeuLysSerAla-----AspPheLeuLysGlu 390
Db 1392 ACATCATGGAAGACAAACCTCTGTACGAAAGGTATCTGAGGAATGCTCTGGAANAAT 1451
Qy 391 IleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
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Qy 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
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Qy 431 TyraAsnValAspAsnThrArgIleLeuLysThrTyraHisSerSerAsnIleSerAsn 450
Db 1572 TATGGGCCAGATGATGTGGCTTGGAAAACTGTATATATATATGATGATGATCATTTGAT 1631
Qy 451 ThrAspTyraLeuArgLeuAlaValGluAspPheTyraThrCysGlnSerIleTyraArgGlu 470
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Db 1632 GAAAGTATTAGAACTACGGAACGGACTTCATTAAGGTGAGTCTATACACCAACA 1691
Qy 471 GluLeuLysGlyLeuGluArgTrpValValGluAsnLysLeuAspGlnLeuLysPheAla 490
Db 1692 GAGCTTCAAGATCTTCCGAAGTGGTGGAAATCATCCGGTTTCACGGATCTGAATTCAC 1751
Qy 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
Db 1752 CCGTGGCGGTGACCGGAAATATATTCTCACGGCATCTTTATCTTTGAGCCCGAGTTT 1811
Qy 511 SerAspAlaArgIleSerTrpAlaLysAsnGlyIleLeuThrThrValValAspPhe 530
Db 1812 TCTAAGTCAGAGAGGTTTATACAAAACCTTCCAATTCCTGTTATTTAGATGATCTT 1871
Qy 531 PheAspIleGlyGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrp 550
Db 1872 TATGACGCCCATGATCTTTAGACGATCTTAAGTTCTTCACAGAATCAGTCAAAAGATGG 1931
Qy 551 AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
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Qy 591 SerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrp 610
Db 2049 GGTACATCTCAAAATGTTTGGAAAGTCCAACTTGAAGCTTTACACGAAAGACGAGATGG 2108
Qy 611 ThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPhe 630
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Db 2169 GCATTTGGGAACAGTCTGTTCTCATAGTCTCTTTTCACTGGGAGGTTCTTACAGATGAA 2228
Qy 651 IleValGluSerSerGluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArg 669
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RESULT 13

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US-09-893-820-55
; Sequence 55, Application US/09893820
; Patent No. 6890752
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 68907521, Joseph P.
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; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-893-820-55
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Alignment Scores:
Pred. No.: 2,89e-110 Length: 2861
Score: 1062.50 Matches: 261
Percent Similarity: 50.6% Conservative: 148
Best Local Similarity: 32.3% Mismatches: 339
Query Match: 25.8% Indels: 61
DB: 3 Gaps: 17
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US-10-041-018-383 (1-784) x US-09-893-820-55 (1-2861)

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Qy 24 IleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleAsp 43
Db 297 ATCGATTCTCTAACGTCATCTCACAGGTTGCAGCATCAGACGAGAGCGT---ATCGAG 353
Qy 44 ThrThrLysGluArgIleGlnLysGlnPheLysAsnVal-----GluLeuSerVal 60
Db 354 ACATTAATATCCAGATTAAAGAAATATGTTAGATGTATGGGCTATGCGCAACGAATCCC 413
Qy 61 SerSerTyrAspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerPro 80
Db 414 TCTGCATATGACACTGCTTTGGGTAGCAAGGATTCAGAGATTCCAGCATGGTCTGCAACACCT 473
Qy 81 CysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGly 100
Db 474 CACTTCTCTGACGCGTTGAATGGATTCTTCAAAATCACTTGAAGATGGTCTTGGGT 533
Qy 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLysAspSerLeuSerSerThr 120
Db 534 -----GAAGGATTCTACTTCTTGGCATATGACAGAATACTGGGTACA 575
Qy 121 LeuAlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGly 140
Db 576 CTTGCATGTATTATTATCCCTTACCTCTGGCGTACTGCGGAGACACAAGTACAGAAAGGT 635
Qy 141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnPro---SerPro 159
Db 636 ATTGAATCTTCAGGACACCAAGCTGGAAGATGGAAGATGAAGCTCATAGTACAGCCA 695
Qy 160 IleGlyPheAspIleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsn 179
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Qy 180 LeuLeuSerLysGlnThrAspPheSerLeuMetLeuHisArgGluLeuGluGlnLys 199
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Db 936 CTCAGCTCTCCGCATCTACAGCGCTGATTATCATGGGTACAGGACAAACAAAGTGTCTG 995
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Qy 317 -----GluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg 331
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Db 1236 ATCTTGAGATTACATGATACAATGATCTCTCAGATGTTTTTAAAAACATTTAGAGATGAG 1295
Qy 352 LeuAlaLeuLysAspGluTyrAlaAla----- 360
Db 1296 -----AATGGGAGTCTTTTGTCTTGGTCCAAACACAGAGAGGATTACAGAC 1346
Qy 361 ---LeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLys 379
Db 1347 ATCTTAAACGTCATCGTTTGCATGTTTTCATTT-----CCGGGAGAA 1391
Qy 380 GlnIleLeuLysSerAla-----AspPheLeuLysGlu 390
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Qy 391 IleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
Db 1452 GTGGATGCCCTTTCACAAATGGGCTTTTAAAGAAATATTCCGGGAGAGGTAGATGCA 1511
Qy 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
Db 1512 CTCAAATATCCCTGGCATAGATGATGCCAAGGTGAGGCTAGAGCTATATTGAAAC 1571
Qy 431 TyrAsnValAspAsnThrArgIleLeuLysThrTyrHisSerSerAsnIleSerAsn 450
Db 1572 TATGGGCCGATGATGTGCTTGGAAACAACTGTATATATGATGATGATGATGATGAT 1631
Qy 451 ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu 470
Db 1632 GAAAGATTTTAGAATAGGAACTGAGTTCATTAAGGTGAGTGTATACACCAACA 1691
Qy 471 GluLeuLysGlyLeuGluArgTyrValValGluAsnLysLeuAspGlnLeuLysPheAla 490
Db 1692 GAGCTTCAAGATCTTCGAAGGTGCTGGAATATCATCCGTTTACGGATCTGAAATTTCACT 1751
Qy 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
Db 1752 CGTGAAGCGGTGAGCGGAATATATTCTCAGCGCATCTCTTTATCTTTGAGCCGAGTTT 1811
Qy 511 SerAspAlaArgIleSerTyrAlaLysAsnGlyIleLeuThrThrValValAspAspPhe 530

Db 1812 TCTAAGTCGACAGAGGTTTATACAAAACTTCCAAATTTCACTGTTATTTTAGATGATCTT 1871
Qy 531 PheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTyr 550
Db 1872 TATGACGCCCATGATCTTTAGACGATCTTAAGTTGTTCAAGATCAGTCAAAAGATGG 1931
Qy 551 AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
Db 1932 GATCTATCACTA---GTGGACCAATGCCCAACAATGAATATATCTTTTGTGGTTTC 1988
Qy 571 LysAspAlaIleCysTyrIleGlyAspGluAlaPheLysTyrGlnAlaArgAspValThr 590
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Qy 591 SerHisValIleGlnThrTyrLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTyr 610
Db 2049 GGCTACATCTCAAAATGTTTGGAAAGTCCCACTTGAAGCTTACACGAAGAAGCAATGG 2108
Qy 611 ThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPhe 630
Db 2109 TCTGAAGCTAAATATGTCATCTTCATGATGATGATGATGATGATGATGATGATGAT 2168
Qy 631 AlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLysLeuSerGluGlu 650
Db 2169 GCATTGGGAACAGCTGCTTCTCATTTGCTCTTTTCACTGGGAGGTTCTTACAGATGAA 2228
Qy 651 IleValGluSerSerGluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArg 669
Db 2229 GTACTCTCCAAATGATGTCGCAATCTAGATTTCTTCACTCATGGCTTTAACAGGCGCT 2288
Qy 670 LeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaVal 689
Db 2289 TTGGTGAATGACACCAAACTTATCAGCGAGAGAGGTCAGGTGAGGTG---GCTTCT 2345
Qy 690 AlaLeuHisLeuSerAsnGlyGluSerGlyLysVal---GluGluGluValValGluGlu 708
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Qy 709 MetMetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsn 728
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Qy 729 GlySerIleValProArgAlaCysLysAspAlaPheTyrAsnMetCysHisValLeuAsn 748
Db 2457 AATACAAAATACCGATATTTCACAAAGAGCTGTTTTTCAAACTGCAAGAAATATGCAA 2516
Qy 749 PhePheTyrAlaAsnAspAspGlyPheThr-----GlyAsnThrIleLeuAspThr 765
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RESULT 14

US-10-041-007-3
; Sequence 3, Application US/10041007
; Patent No. 6946283
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthese
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis

US-10-041-007-3

Alignment Scores:

Pred. No.: 2,89e-110 Length: 2861
Score: 1062.50 Matches: 261
Percent Similarity: 50.6% Conservative: 148
Best Local Similarity: 32.3% Mismatches: 339
Query Match: 25.8% Indels: 61
DB: 3 Gaps: 17

US-10-041-018-383 (1-784) x US-10-041-007-3 (1-2861)

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DQ : : : : :
Db ATCGATTCTTACGTCATCTTCAAGGTTGCGATCAGACAGAGCGT---ATCGAG 353
QY 44 ThrThrLysGluArgIleGlnLysGlnPheLysAsnVal-----GluIleSerVal 60
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QY 61 SerSerTyrAspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerPro 80
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QY 81 CysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGly 100
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QY 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLysAspSerLeuSerSerThr 120
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QY 121 LeuAlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGly 140
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QY 141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnPro---SerPro 159
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QY 352 LeuAlaLeuLysAspGluTyrAlaAla----- 360
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QY 361 ---LeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerGlyLys 379
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DQ : : : : :
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Db GTGGATGCCCTTTGCAAAATGGGCTTTTAAAGAAATATTCGGGGAGAGTAGATGCA 1511
QY 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
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Db TATGGGCCAGATGATGTGTGGCTTGGAAAACTATATATATGATGTCATACATTTCCAA 1631
QY 451 ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu 470
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QY 471 GluLeuLysGlyLeuGluArgTrpValValGluAsnLysLeuAspGlnLeuLysPheAla 490
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QY 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
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QY 531 PheAspIleGlyGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrp 550
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QY 551 AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
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Db GGTACATTTCAAAATGTTTGGAAAGTCCAACTTGAAGCTTTACACGAAGAAAGCAGAATGG 2108
QY 611 ThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPhe 630
DQ : : : : :
Db TCTGAAGCTTAAATATGTGCGCATCTTCAATGAATACATAGAGAATCGGATGTGTCAAT 2168
QY 631 AlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLysLeuSerGluGlu 650

Db 2169 GCATTGGGAACAGTCGTTCTCATTAGTGCTCTTTTCACTGGGAGGTTTCTACAGATGAA 2228
Qy 651 IleValGluSerSerGluTyHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArg 669
Db 2229 GTACTCTCCAAATGATCGGAATCTAGATTTCTTCACTCATGGCTTAAACAGGCGT 2288
Qy 670 LeuLeuAsnAspIleHisSerPheLeuArgGluPheLysGluGlyLysLeuAsnAlaVal 689
Db 2289 TTGTGTAATGACACCAAACTTATCAGCGCAGAGAGGTCAAGGTGAGGTG---GCTTCT 2345
Qy 690 AlaLeuHisLeuSerAsnGlyGluSerGlyLysVal---GluGluGluValValGluGlu 708
Db 2346 GCCATCAATGTTATATGAAGGACCATCTCTAAATCTCTGAAGAAGAGCTTACACAT 2405
Qy 709 MetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuLysPheGluGluAsn 728
Db 2406 GTCTATAGTGTCTAGGAATGCGCTCGAAGAGTTGAATAGG-----GAGTTTGTG 2456
Qy 729 GlySerIleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsn 748
Db 2457 AATAACAAATACCGGATATTTACAAAGAGCTGTTTTGAAACTGCAAGAATAATGCAA 2516
Qy 749 PhePheTyralaAsnAspAspGlyPheThr-----GlyAsnThrIleLeuAspThr 765
Db 2517 CTCTTTATATGCAAGGGGATGGTTTGACACTATCATGATATGGAATTTAAAGAGCAT 2576
Qy 766 ValLysAspIleIleTyAsnProLeu 774
Db 2577 GTCAAAATTTGCTCTCTTCAACACGATT 2603

RESULT 15

US-10-041-007-38

; Sequence 38, Application US/10041007

; Patent No. 6946283

; GENERAL INFORMATION:

; APPLICANT: Matsuda, Seiichi P.T.

; APPLICANT: Schepmann, Hala G

; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

; FILE REFERENCE: P02081US1

; CURRENT APPLICATION NUMBER: US/10/041,007

; CURRENT FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: US 60/259,881

; PRIOR FILING DATE: 2001-01-05

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 38

; LENGTH: 2241

; TYPE: DNA

; ORGANISM: Ginkgo biloba

US-10-041-007-38

Alignment Scores:

Pred. No.:	1,78e-109	Length:	2241
Score:	1054.00	Matches:	253
Percent Similarity:	51.2%	Conservative:	145
Best Local Similarity:	32.6%	Mismatches:	306
Query Match:	25.6%	Indels:	74
DB:	3	Gaps:	13

US-10-041-018-383 (1-784) x US-10-041-007-38 (1-2241)

Qy 33 GlyGlnThrAsnProThrAsnLeuIleAspThrThrLysGluArgIleGlnLysGln 52
Db 22 GGTGAACGAAATCCA----- 36
Qy 53 PheLysAsnValGluIleSerValSerTyAspThrAlaTrpValAlaMetValPro 72
Db 37 -----TCTGCATATGATACAGCTTGGGTGGCAAGAAATTCG 72
Qy 73 SerProAsnSerProLysSerProCysPhePheProGluCysLeuAsnTrpLeuIleAsnAsn 92
Db 73 TCAATTGACGGCTCTGGTGACCCCAATTTCCCAACAGCTTCAATGGATTCTGAACAAAT 132

Qy 93 GlnLeuAsnAspGlySerTrpGlyLeuValAsnHisThrHisAsnHisAsnHisProLeu 112
Db 133 CAACTGCCAGATGGCTCGTGGGT-----GAGGAGTGCATTTTCTGT 174
Qy 113 LeuLysAspSerLeuSerSerThrLeuAlaCysIleValAlaLeuLysArgTrpAsnVal 132
Db 175 GCCTATGACAGAGATTTTAAACACTCTCGCTGCTCTCTCACTCTCAAAATATGGAATAAG 234
Qy 133 GlyGluAspGlnIleAsnLysGlyLeuSerPheIleGluSerAsnLeuAlaSer--Ala 151
Db 235 GCGCAGATTCACTGAGAGAGGGTGTGTTGTGAGAAAACACATGGAGAAATGAAG 294
Qy 152 ThrGluLysSerGlnProSerProIleGlyPheAspIleIlePheProGlyLeuLeuGlu 171
Db 295 GACGAAGCTGACAATCACAGGCCAAGTGGATTGAGGTGCTGTTTCTCGCAATGTAGAT 354
Qy 172 TyrAlaLysAsnLeuAspIleAsnLeuLysGlnThrAspPheSerLeuMetLeu 191
Db 355 GAAGCAAAAGCTTGGGATTGGATCTTCTTATCACCTCCCTTCTATCTCCCAATCCAC 414
Qy 192 HisLysArgGluLeuGlnLysArgCysHisSerAsnGluMetAspGlyTy- 209
Db 415 CAAAAGCGCCAGAAAAGCTTCAAAAGATTTCCCTCAATGTTCTTCAACACCTCAGACG 474
Qy 210 ---LeuAlaTyIleSerGluGlyLeuGlyAsnLeuTyAspTrpAsnMetValLysLys 228
Db 475 GCGTTGCTCTACTCTCTGGAGGGTTTGCAGAGTGTGGTGGACTGGCAAGAGATCACAAAT 534
Qy 229 TyrGlnMetLysAsnGlySerValPheAsnSerProSerAlaThrAlaAlaPheIle 248
Db 535 CTTCAATCAAGAGACGATCAATTTTAAAGCTCCCTGCTACTACTGCTGCTGCTTCATG 594
Qy 249 AsnHisGlnAsnProGlyCysLeuAsnTyLeuAsnSerLeuLeuAspLysPheGlyAsn 268
Db 595 CACACTCAAAACAAACAGTCCCTCCACTTCTCACTGCTGCTCAGCAATTTGGCGAC 654
Qy 269 AlaValProThrValTyProHisAspLeuPheIleArgLeuSerMetValAspThrIle 288
Db 655 TACGTTCTTGGCCATTACCACCTTGATCTATTTGAACGCTCTGGGCTGCTGATACAGTT 714
Qy 289 GluArgLeuGlyIleSerHisPheArgValGluIleLysAsnValLeuAspGluThr 308
Db 715 GAACGCTTGGGAATCGATCGCTATTTCAAGAAAGAAATCAAGAAATCTCTGGATTACGTT 774
Qy 309 TyArgCysTrp---ValGluArgAspGlu-----GlnIlePheMetAsp 322
Db 775 TATAGGTACTGGGACCGCCGAAAGAGCGTGGGATGGCAAGATGCAATCTCTTCTGTAT 834
Qy 323 ValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsnGlyTyArgValSerPro 342
Db 835 GTCGATGACACTGCCATGGGTCTTAGAATCTGAGACTTCATGATACATATGTATCTTCA 894
Qy 343 AspProLeuAlaGluIleThrAsnGlu----- 351
Db 895 GATGTTCTGAGAAATTTCAAGACGAGAAAGGAGACTTCTTTTGTCTTGGCGGTCAAAACG 954
Qy 352 ---LeuAlaLeuLysAspGluTyArgAlaAlaLeuGluThrTyHisAlaSerHisIleLeu 370
Db 955 CAAATTGGTGTGACCGATAAT-----CTTAACCTTTTATAGATGTTTCAAGATATGT 1005
Qy 371 TyrGlnGluAspLeuSerSerGlyLysGlnIleLeuLysSerAla----- 385
Db 1006 TTT-----CCGGGAGAAAAGATAATGGAAGACCTAAGACCTTCACTTACA 1050
Qy 386 -----AspPheLeuLysGluIleIleSerThrAspSerAsnArgLeuSerLys 401
Db 1051 AATCATCTCCAAATGCTCTTGCCAAAAACAACGCAATTTTGAATGAGTGGGTGCTCAAGAG 1110
Qy 402 LeuIleHisLysGluValGluAsnAlaLeuLysPheProIleAsnThrGlyLeuGluArg 421
Db 1111 GATCTTCTGGAGAGTGGAGTATGCTATATAAGATATCCCGGGCATAGAGATGCCAAGA 1170
Qy 422 IleAsnThrArgAsnIleGlnLeuTyAsnValAspAsnThrArgIleLeuLysThr 441

Job time : 437.242 secs

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Db      1171  TTGGAGGCAAGAAGTTACATAGACAAATTTGGATCAAATGATGCTCGGCTGGGGAAGACT 1230
Qy      442  ThrTyrHisSerSerAsnIleSerAsnThrAspTyrLeuArgLeuAlaValGluAspPhe 461
Db      1231  GTGTATAAGATGCTATATGTGAGCAACGAAANAATTTGGAGCTGGCCAAATTTGGACTTC 1290
Qy      462  TyrThrCysGlnSerIleTyrArgGluGluLeuLeuGlyLeuGluArgTrpValValGlu 481
Db      1291  AATATGCTGCGAGCCCTTACACCAAAAGAGACTCAACACATTTGTCAGCTGGTGGAGAA 1350
Qy      482  AsnLysLeuAspGlnLysPheAlaArgGlnLysThrAlaTyrCysTyrPheSerVal 501
Db      1351  TCGGGATTCAATGATCTTACATTCACCCGCGAGCCCTGTGGAATGATTTCTCAGTG 1410
Qy      502  AlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLysAsnGly 521
Db      1411  GCGGTTAGTATGTTTGGAGCCAGAAATTCGCTGTGTAGAATTGCCTATGCCAAGACTTCT 1470
Qy      522  IleLeuThrThrValValAspAspPhePheAspIleGlyGlyThrIleAspGluLeuThr 541
Db      1471  TGCCTCGCAGTTATTCTAGACGATCTTACGACCCACCGGATCTCTGGATGATCTTAAA 1530
Qy      542  AsnLeuIleGlnCysValGluLysTrpAsnValAspValAspLysAspCysCysSerGlu 561
Db      1531  TTGTTCTCTGAAGCGTCCGAGATGGGATATCTCTGTCTGGATAGCGTTCGGGATAAT 1590
Qy      562  HisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAspGluAla 581
Db      1591  CAGTTGAAAGTTTGTCTTCTAGGGCTGTACAACACAGATGAATGGATTTGGAAAAGATGA 1650
Qy      582  PheLysTrpGlnAlaArgAspValThrSerHisValIleGlnThrTrpLeuGluLeuMet 601
Db      1651  CTCAGGACAACAGCGCGTGTGCTGGGCTATCTTCGAAAAGTATGGAGGGCTTGCCTC 1710
Qy      602  AsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyrValProThrLeuAsnGlu 621
Db      1711  GCATCGTATACCAAGAACCGGATGGTCGGCAAGTAATGTGCGGACATTCGACATTCACAA 1770
Qy      622  TyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIleValLysProAlaIleTyr 641
Db      1771  TATGTGAAAATGSCAAAGTGTCATAGCACATTCGACAGTCGTACTAAACTCAATCTTT 1830
Qy      642  PheValGlyProLysLeuSerGluGluIleValGluSerSerGluTyrHisAsnLeuPhe 661
Db      1831  TTCACCTGGAGAAATTACTTCTCGATTATTTACAGCAAGTAGACCTTCGGTCCAAATTT 1890
Qy      662  ---LysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIleHisSerPheLysArgGlu 680
Db      1891  CTGCATCTTTGTGCTTTTGACTGGACGACTAATCATGACACCCAGACTTACCGCCGAG 1950
Qy      681  PheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSerGlyLys 700
Db      1951  AGAAACCGTGGTGAATTTGTTTCCAGCGTACAGTG-CTACATGAGGGAAAAATCCGGAGTG 2009
Qy      701  -ValGluGluGluValValGluMetMetMetMetIleLysAsnLysArgLysGluLe 720
Db      2010  CACAGAGGAAGAGCTCTAAGTCATGTTATGTTATCATCATCGACACGCACTGAAGGAAT 2069
Qy      720  uMetLysLeuIlePheGluAsnGlySerIleValProArgAlaCysLysAspAlaPh 740
Db      2070  G---AATGGGAGTTGGCCACCCAGGAGCAATGCCCATTTGTGTGTGAGAGAGACTGCT 2126
Qy      740  eTrpAsnMetCysHisValLeuAsnPhePheTyrAlaAsnAspAspGlyPhe-----Th 758
Db      2127  GTTCAACACTGCAAGAGTGATCGAGCTGTTTATATATGTATGACAGAGATGGCTTTGGTATCTC 2186
Qy      758  rGlyAsnThrIleLeuAspThrValLysAspIleIleTyrAsnProLeu 774
Db      2187  TGACAAAGAGATGAAGACCATGTGACCGCACTCTTTTCGATCTCTGTG 2235
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Search completed: February 16, 2006, 08:16:49

Result No.	Query			Description	
	Score	Match	Length	ID	Description
1	44.4	1.6	662	6	US-09-925-065A-34903
2	44.2	1.6	564	6	US-09-925-065A-33058
C 3	44.2	1.6	684	6	US-09-925-065A-708441
	44.2	1.6	4023	12	US-11-098-686-9790
C 5	44.2	1.6	1457619	12	US-11-098-686-8790
6	44	1.6	662	6	US-09-925-065A-34904
C 7	42.6	1.5	534	6	US-09-925-065A-34904
8	42.6	1.5	182190	12	US-11-121-086-102
9	42	1.5	3942	9	US-11-245-147-216
10	42	1.5	3949	9	US-11-072-175-2
11	41.6	1.5	610	6	US-09-925-065A-334949
C 12	41.4	1.5	513	6	US-09-925-065A-200626
C 13	41.4	1.5	534	6	US-09-925-065A-589469
14	41.4	1.5	1230	8	US-10-793-626-3257
15	41.4	1.5	1434	8	US-10-793-626-3249
16	41.4	1.5	3410	8	US-10-793-626-3505
17	41.4	1.5	3800	8	US-10-793-626-4321
18	41.4	1.5	3818	8	US-10-793-626-3367
19	41.2	1.5	1903	8	US-10-750-185-45082
20	41.2	1.5	1303	8	US-10-750-623-45082


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Db      171 ACTGATTTGACACTTAAATAAGTTTAAATGTTAAATTTTATGTCATCTATATTTTGTGTC 230
QY      2766 CTTAAAAAATAAAAAAATAAAAAA 2791
Db      231 ACAATTTAAAAATAAAAAATAAATAACA 256

RESULT 2
US-09-925-065A-830598
; Sequence 830598, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 830598
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-830598

Query Match          1.6%; Score 44.2; DB 6; Length 564;
Best Local Similarity 47.6%; Pred. No. 9.5; Indels 5; Gaps 1;
Matches 166; Conservative 0; Mismatches 178;

QY      720 AAACAACAGATTTTGTGATGCTACATAAGAGGGAATTCGAGCAAAAAGATGCCAT 779
Db      203 AGCAGACATAATTTAAAAACATTTTAAACATGGGAAGAGAGTTTCCCAATATCAT 262
QY      780 TCAATAGAGATGGATGATCTTGGCGTATATCTCTGAAGGACTCGGTAAATTTATATGAT 839
Db      263 CATATAGTTTGGTTGAAGAGTGAACAAATACAGAGATGCTCAACAGAAATATAATTAC 322
QY      840 TGAATATGCTGAAGAAATATCAGATGAAAGATGGTTCTTCACTCACCATCAGCA 899
Db      323 AGCCAGATGGTGATGATTTTGTGAGATATCTATTTGCTTTGATTAATCAACACCGGCA 382
QY      900 ACAGCTGCTGCTTTCAATTAATCATCAAAATCCTGGTTGCTTAATTTAAATTCACTT 959
Db      383 CCTTTTGTACGTTCACTGATATTTGAGAGATATATAGTGCCAAATCTGTATAGTATCTG 442
QY      960 TTGGCAAGTTTGGTAATCAGTCCC-----AACAGTTTATCTCATGATTTTATTTATCC 1014
Db      443 TTTTCTTTCTTTTTCACCCCTGGTAATAAGATTTATTCCTAACTAAGTTTTCCTCC 502
QY      1015 GACTTTCTATGTTGACACAATTTGAAGATTTAGGAATTTTCAACCATTT 1063
Db      503 CACTTATTTTAGTTTGTATATAAAATTTGGAAGTAGCTATTTTCAACATCT 551

RESULT 3
US-09-925-065A-708441/c
; Sequence 708441, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome

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; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 708441
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-708441

Query Match          1.6%; Score 44.2; DB 6; Length 684;
Best Local Similarity 47.6%; Pred. No. 10; Indels 5; Gaps 1;
Matches 166; Conservative 0; Mismatches 178;

QY      720 AAACAACAGATTTTGTGATGCTACATAAGAGGGAATTCGAGCAAAAAGATGCCAT 779
Db      358 AAGCAGACATAATTTAAAAACATTTTAAACATGGGAAGAGAGTTTCCCAATATCAT 299
QY      780 TCAATAGAGATGGATGATCTTGGCGTATATCTCTGAAGGACTCGGTAAATTTATATGAT 839
Db      298 CATATAGTTTGGTTGAAAGTGAACAAATACAGAGATGCTCAACAGAAATATAATTAC 239
QY      840 TGAATATGCTGAAGAAATATCAGATGAAAGATGGTTCTGTTTCAACTCACCATCAGCA 899
Db      238 AGCCAGATGGTGATGATTTGTGAGATATCTATTTGCTTTGATTAATCAACACCGGCA 179
QY      900 ACAGCTGCTGCTTTCAATTAATCATCAAAATCCTGGTTGCTTAATTTAAATTCACTT 959
Db      178 CCTTTTGTACGTTCACTGATGAATATTTGAGAGTAAATATAGTGCCAAATCTGTATAGTATCTG 119
QY      960 TTGGCAAGTTTGGTAATGACGTCCC-----AACAGTTTATCTCATGATTTTATTTATCC 1014
Db      118 TTTTCTTTCTTTTTCACCCCTGGTAATAAGATTTATTCCTAAGTTTTCCTCC 59
QY      1015 GACTTTCTATGTTGACACAATTTGAAGATTTAGGAATTTTCAACCATTT 1063
Db      58 CACTTATTTTAGTTTGTATATAAAATTTGGAAGTAGCTATTTTCAACATCT 10

RESULT 4
US-11-098-686-9790
; Sequence 9790, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9790
; LENGTH: 4023
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-11-098-686-9790

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Query Match      1.6%; Score 44.2; DB 12; Length 4023;
Best Local Similarity 51.8%; Pred. No. 20;
Matches 100; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 543 ATTGTTGCATTAAGAGATGGAATGTTGGGGAAGATCAATAATAAAGTCTAAAGTTT 602
Db 3073 ACTACTACACATAAAAAATTTACAACCTTGCTTAAATAATAGAAAAAATCTTGGCTCCCTC 3132

QY 603 ATTGAGTCAATCTTGCTTCAGCTACTGAAAAAAGTCAACCATCTCCCATTTGTTTGAC 662
Db 3133 AATAAATCTACTATGAAATACTAATAATTATAGAGCACTACAGCTCTAAATCTTAC 3192

QY 663 ATCATATTTCTGTTGCTTGAGTATGCGAAAAAATTTGGACATAAACCCTCTCTTCAAAA 722
Db 3193 ACTGTAATTTACTTCTATAAATAAGTATACCCTAACTTAGAAAAACCAACTCCGTTGAGCA 3252

QY 723 CAACACAGATTTTA 735
Db 3253 CAAGCAGGTATTA 3265

RESULT 5
US-11-098-686-8739/c
; Sequence 8739, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/416,395
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8739
; LENGTH: 1457619
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-11-098-686-8739

Query Match      1.6%; Score 44.2; DB 12; Length 1457619;
Best Local Similarity 51.8%; Pred. No. 1.6e+02;
Matches 100; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 543 ATTGTTGCATTAAGAGATGGAATGTTGGGGAAGATCAATAATAAAGTCTAAAGTTT 602
Db 1107099 ACTACTACACATAAAAAATTTACAACCTTGCTTAAATAATAGAAAAAATCTTGGCTCCCTC 1107040

QY 603 ATTGAGTCAATCTTGCTTCAGCTACTGAAAAAAGTCAACCATCTCCCATTTGTTTGAC 662
Db 1107039 AATAAATCTACTATGAAATACTAATAATTATAGAGCACTACAGCTCTAAATCTTAC 1106980

QY 663 ATCATATTTCTGTTGCTTGAGTATGCGAAAAAATTTGGACATAAACCCTCTTCAAAA 722
Db 1106979 ACTGTAATTTACTTCTATAAATAAGTATACCCTAACTTAGAAAAACCAACTCCGTTGAGCA 1106920

QY 723 CAACACAGATTTTA 735
Db 1106919 CAAGCAGGTATTA 1106907

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RESULT 6
US-09-925-065A-34904
; Sequence 34904, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome

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; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34904
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-34904

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Query Match      1.6%; Score 44; DB 6; Length 662;
Best Local Similarity 50.5%; Pred. No. 11;
Matches 104; Conservative 1; Mismatches 101; Indels 0; Gaps 0;

QY 2586 GTATAATAAGGTTGTAGTTGTATATAATAAGGTAATAGGTAATCAATAGAAAGCTTAAGT 2645
Db 51 GTTTCATATATTTTGTATGGCAGCAACAAATGAAGTAGGATATCATATTAGTATGCCAATTA 110

QY 2646 TATTAAGTTTTTCCCTCGTGTCACACCGTGAGGTTCTTTGTTAAAGCAGTTTATTTAT 2705
Db 111 TTTTAAATAATAAAACCAAGGCAAGAGAATAATGTTACAATGTAATAATAATTAATAAT 170

QY 2706 GTTACTAGCAGACCTTGGTGGTTGTTGCTGTTTATCTCTAAGAGCCTTTCACCTTTGTT 2765
Db 171 ACTGAATTTGTACACTTTAAAAAATGTTAAAAATGTTAAATTTTGTGTCATATATTTTGTG 230

QY 2766 CTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAA 2791
Db 231 ACATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAA 256

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RESULT 7
US-09-925-065A-589470/c
; Sequence 589470, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 589470
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-589470

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Query Match      1.5%; Score 42.6; DB 6; Length 534;
Best Local Similarity 46.2%; Pred. No. 20;

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; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24

Db 354 ACCTAGAACATTAAATCTCGTAGTTAAGTAAATGTTTGGCTATAAATGTCAGGCACTGTG 295

QY 542 TATTGTTGCAATTAATAAGATGGAATGTTGGGGAAGATCAATAATAAAGGCTTAAGTTT 601
| | | | |
Db 294 TCTCGTTGCAAAATTAGAGTGTGAGGAGGCGAGCTAACTTGAAATTACAAATGATTTG 235
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QY 602 TATTGAGTCAAACTTGTCTTACGCTACTGAAAAAGTCAACCATCTCCCATTTGTTTGA 661
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Db 234 TATTAAATTAACATCTCTTGAGTTCAGAAATTAATTTCCAAACACTTAAACTGTTTITTA 175
| | | | |
QY 662 CATCATATTTCTCGTTTCTTGTGATATCGAAAAACTTGGACATAAACTCTCTTTCAA 720
| | | | |
Db 174 TCTGCGATTCTCGAGTTCTTTTGTAGTTACATTCAGTAGGAATCGGATTTTTTTTAA 116
| | | | |

RESULT 14

US-10-793-626-3257
; Sequence 3257, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3257
; LENGTH: 1230
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3257

Query Match 1.5%; Score 41.4; DB 8; Length 1230;
Best Local Similarity 47.2%; Pred. No. 50;
Matches 126; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 530 AACATTAGCATGTATGTTGCATTAATAAGATGGAATGTTGGGGAAGATCAATAATAA 589
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Db 939 AATAGTAATAGATTTATCTTAAATGAAGCCGAGAAATCAGTCTGTTGATAATGATAA 998
| | | | |
QY 590 AGGTCTAAGTTTTTATGAGTCAAACTCTGCTTCACTGAAAAAGTCAACCATCTCC 649
| | | | |
Db 999 AACTGTAATTTTACCGATTAGTAACAAGAGAAAGTTCTAACAAAGGTAATACACCAA 1058
| | | | |
QY 650 CATTTGGTTTTGACATCATATTTCTCGTTGTTGATGCGAAAAAAGTCTGGACATAAA 709
| | | | |
Db 1059 AGTAAGTAAAAAATAAATAAGAGGTATGAATGATAATGTTTACCATTTAATGGTAATA 1118
| | | | |
QY 710 CCTCCTTTCAAAACAAACAGATTTTGTGCTTACATAAGAGGGAATTTGGACAAAA 769
| | | | |
Db 1119 ATTGATCTCTAAAGAAATAGATTTTACACAAAAGTTTAAACCAAGAAAGTATGGGAAT 1178
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QY 770 AAGATGCCATTCAAATGAGATGGATGG 796
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Db 1179 TGAAAACGTCAAAGATAAATGGGTGG 1205
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RESULT 15

US-10-793-626-3249
; Sequence 3249, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3249
; LENGTH: 1434
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3249

Query Match 1.5%; Score 41.4; DB 8; Length 1434;
Best Local Similarity 47.2%; Pred. No. 52;
Matches 126; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 530 AACATTAGCATGTATGTTGCATTAATAAGATGGAATGTTGGGGAAGATCAATAATAA 589
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Db 939 AATAGTAATAGATTTATCTTAAATGAAGCCGAGAAATCAGTCTGTTGATAATGATAA 998
| | | | |
QY 590 AGGTCTAAGTTTTTATGAGTCAAACTCTGCTTCACTGAAAAAGTCAACCATCTCC 649
| | | | |
Db 999 AACTGTAATTTTACCGATTAGTAACAAGAGAAAGTTCTAACAAAGGTAATACACCAA 1058
| | | | |
QY 650 CATTTGGTTTTGACATCATATTTCTCGTTGTTGATGCGAAAAAAGTCTGGACATAA 709
| | | | |
Db 1059 AGTAAGTAAAAAATAAATAAGAGGTATGAATGATAATGTTTACCATTTAATGGTAATA 1118
| | | | |
QY 710 CCTCCTTTCAAAACAAACAGATTTTGTGCTTACATAAGAGGGAATTTGGACAAAA 769
| | | | |
Db 1119 ATTGATCTCTAAAGAAATAGATTTTACACAAAAGTTTAAACCAAGAAAGTATGGGAAT 1178
| | | | |
QY 770 AAGATGCCATTCAAATGAGATGGATGG 796
| | | | |
Db 1179 TGAAAACGTCAAAGATAAATGGGTGG 1205
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 06:36:26 ; Search time 2408.27 Seconds
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Title: US-10-041-018-361
Perfect score: 2792
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2582.6	92.5	3117	7	US-10-041-018-362
3	1428.6	51.2	2594	7	US-10-041-018-368
4	809.4	29.0	2638	7	US-10-041-018-367
5	782.2	28.0	2658	7	US-10-041-018-378
6	782.2	28.0	2658	7	US-10-041-018-381
7	732.4	26.2	2506	7	US-10-041-018-377
8	561.2	20.1	2554	7	US-10-041-018-3441
9	559.6	20.0	2716	8	US-10-041-018-3441
10	466	16.7	2730	8	US-10-041-018-3441
11	433.2	15.5	2086	7	US-10-041-018-17004
12	430	15.4	2364	8	US-10-041-018-175619
13	392.4	14.1	2029	7	US-10-041-018-5988
14	379.4	13.6	2223	6	US-10-041-018-107
15	357.4	12.8	2178	8	US-10-041-018-177869
16	356.4	12.8	2070	7	US-10-041-018-19081
17	330	11.8	1559	7	US-10-041-018-375
18	315.6	11.3	3666	7	US-10-041-018-72152
19	288.8	10.3	1150	7	US-10-041-018-729
20	276.8	9.9	1008	7	US-10-041-018-2257
21	357.4	12.8	2178	8	US-10-041-018-177869
22	264.8	9.5	2193	7	US-10-041-018-72156
23	241.6	8.7	2313	7	US-10-041-018-36043

ALIGNMENTS

RESULT 1

US-10-041-018-361
; Sequence 361, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 361
; LENGTH: 2792
; TYPE: DNA
; ORGANISM: Stevia rebaudiana
US-10-041-018-361

Query Match	100.0%;	Score 2792;	DB 7;	Length 2792;
Best Local Similarity	100.0%;	Pred. No. 0;		
Mismatches	0;	Mismatches	0;	Indels 0; Gaps 0;
Matches	2792;	Conservative	0;	
QY	1	CCACATCATCTTTTATCAACCAATACCATGTTCTGCGACCGAAGACTGATAGCGACG	60	
DB	1	CCACATCATCTTTTATCAACCAATACCATGTTCTGCGACCGAAGACTGATAGCGACG	60	
QY	61	GACCTGACGACGCGCTTTTATCTCTGTTGGACCACTTAAACAAATTCGACCATCATCT	120	
DB	61	GACCTGACGACGCGCTTTTATCTCTGTTGGACCACTTAAACAAATTCGACCATCATCT	120	
QY	121	ACTCCGGTGGACAGATTTTCAATTTTGCATTTAGTAAATCAGCAAACTAAACATCAATGATC	180	
DB	121	ACTCCGGTGGACAGATTTTCAATTTTGCATTTAGTAAATCAGCAAACTAAACATCAATGATC	180	
QY	181	TTTCACTATGACATCGCGTCCCTTTGTTTAAACCAATCAATCGCGCGGCTCTGTCAG	240	
DB	181	TTTCACTATGACATCGCGTCCCTTTGTTTAAACCAATCAATCGCGCGGCTCTGTCAG	240	
QY	241	CTATTATATGACATCACTTCACTGTTGGAACAACTAATCCACTAATCTGATCATTTG	300	
DB	241	CTATTATATGACATCACTTCACTGTTGGAACAACTAATCCACTAATCTGATCATTTG	300	
QY	301	ATACAACCAAGAACGATCCAAAAACAGTTTAAAAATGTAGAAATTTCTGTTTCTTCAT	360	

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Sequence 365, App
Sequence 373, App
Sequence 491, App
Sequence 167282,
Sequence 30695, A
Sequence 43, Appl
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Sequence 43, Appl
Sequence 363, App
Sequence 170921,
Sequence 96438, A

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301 ATACAAAGAGGATGGATCCAAAAACAGTTTAAAAAATGTAGAAATTTCTGTTTCTTCAT 360
QY
361 ATGACACAGCATGGGTAGCATGGTCCCTTCTCCAAACTCACCCAATCGCCTTGTTCCTC 420
Db
361 ATGACACAGCATGGGTAGCATGGTCCCTTCTCCAAACTCACCCAATCGCCTTGTTCCTC 420
QY
421 CTGAGGTCTCAATGGTTTAAATTAATCAGCTTAATGATGGTTCATGGGTCTTGTGTTA 480
Db
421 CTGAGGTCTCAATGGTTTAAATTAATCAGCTTAATGATGGTTCATGGGTCTTGTGTTA 480
QY
481 ATCAGACTCATATCATATCAACCGTCTGTAAAGATTTCTATCTTCAACATTAGCAT 540
Db
481 ATCAGACTCATATCATATCAACCGTCTGTAAAGATTTCTATCTTCAACATTAGCAT 540
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541 GTATTGTTGCATTTAAAGATGGAATGTTGGGGAAGATCAAAATAAATAAGGTCTAAGTT 600
Db
541 GTATTGTTGCATTTAAAGATGGAATGTTGGGGAAGATCAAAATAAATAAGGTCTAAGTT 600
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Db
601 TTATTGAGTCAATCTTGCTTCAGCTTACTGAAAAAGTCAACCATCTCCCATTTGGTTTG 660
QY
661 ACATCATATTTCTGGTTTGGTTCAGTATCGGAAAACTTGGACATAAACCTCTTTCAA 720
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661 ACATCATATTTCTGGTTTGGTTCAGTATCGGAAAACTTGGACATAAACCTCTTTCAA 720
QY
721 AACAAACAGATTTTGTGTTGCTTACATAAGAGGGAATGGAGCAAAAAAGATGCCATT 780
Db
721 AACAAACAGATTTTGTGTTGCTTACATAAGAGGGAATGGAGCAAAAAAGATGCCATT 780
QY
781 CAAATGAGATGAGTGGATCTTGGGCTATATCTCTGAAGGACTCGGTAAATTTATATGATT 840
Db
781 CAAATGAGATGAGTGGATCTTGGGCTATATCTCTGAAGGACTCGGTAAATTTATATGATT 840
QY
841 GGAATATGTTGAGAAATATCAGATGAAAAATGGTCTCTGTTTCACTCACCATCAGCAA 900
Db
841 GGAATATGTTGAGAAATATCAGATGAAAAATGGTCTCTGTTTCACTCACCATCAGCAA 900
QY
901 CAGCTGCTCTTTCATTATCATCAAAATCCTGGTTGTCTTAATTTTAAATTTCACTTT 960
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901 CAGCTGCTCTTTCATTATCATCAAAATCCTGGTTGTCTTAATTTTAAATTTCACTTT 960
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961 TGGACAAGTTTGGTAAATGCAATCCCAACAGTTTATCCTCATGATTTATTTATCCGACTTT 1020
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961 TGGACAAGTTTGGTAAATGCAATCCCAACAGTTTATCCTCATGATTTATTTATCCGACTTT 1020
QY
1021 CTATGTTGACACAAATTTGAAGATTTAGGAATTTACACCACTTTTCAGAGTGGAAATTA 1080
Db
1021 CTATGTTGACACAAATTTGAAGATTTAGGAATTTACACCACTTTTCAGAGTGGAAATTA 1080
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1081 ATGTTTGTAGATGAACATACAGATGTTGGTGGACAGATGAGCAAAATATTCATGGATG 1140
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Db
1141 TTGTAA CATGTGCTTTAGCCTTTCCGTTTATTAAGGATCAATGGTATGAAGTTTCCCCAG 1200
QY
1201 ATCCATTTGCTGAAATTTACTATGATTTAGCTTTGAAAGCAAGATGAGCTTTGAAA 1260
Db
1201 ATCCATTTGCTGAAATTTACTATGATTTAGCTTTGAAAGCAAGATGAGCTTTGAAA 1260
QY
1261 CATATCATGGCTCACATATATATACCAAGAGGATTTATCTTCTGAAAAACAAATCTTGA 1320
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QY
1321 AGTCAGCTGATTTCTCAAAGAGATATATCCAATGATTTCAACAGGCTTTCTAAATTA 1380
Db
1321 AGTCAGCTGATTTCTCAAAGAGATATATCCAATGATTTCAACAGGCTTTCTAAATTA 1380
QY
1381 TTCAAAAGAGGTGGAAATGCTTAAAGTTCCCTATCAATACCGGTTTAGACGCATAA 1440
Db
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Db
1381 TTCAAAAGAGGTGGAAATGCTTAAAGTTCCCTATCAATACCGGTTTAGAACGCATAA 1440
QY
1441 ACACTAGACGAATATACAGCTTTTCAATGTAGACAAATACAGAAATTTCTGAAAACTACAT 1500
Db
1441 ACACTAGACGAATATACAGCTTTTCAATGTAGACAAATACAGAAATTTCTGAAAACTACAT 1500
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1501 ATCACTCATCAAAATATTAGTAACTGATTAACCTAAGGTTGGCTGTTGAAGATTCTTACA 1560
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QY
1621 AGTTGGACAGCTCAAGTTTGTAGCAAAAAAGACCGCTTACTGTTATTTCTCTGTTGCTG 1680
Db
1621 AGTTGGACAGCTCAAGTTTGTAGCAAAAAAGACCGCTTACTGTTATTTCTCTGTTGCTG 1680
QY
1681 CAAACATTTTCGTTCCCGAATTTATCAGATGCGCGTATTTTCATGGGCCAAAAATGGCATAT 1740
Db
1681 CAAACATTTTCGTTCCCGAATTTATCAGATGCGCGTATTTTCATGGGCCAAAAATGGCATAT 1740
QY
1741 TAACTACAGTACTGATGACTTTTTTTTGATATCGGTGGTACAATCGATGAAATGACCAACC 1800
Db
1741 TAACTACAGTACTGATGACTTTTTTTTGATATCGGTGGTACAATCGATGAAATGACCAACC 1800
QY
1801 TGATTCATGTGTTGAAAAATGGAATGTAGATGTGCAAGGATTTGTTGTTCAAGAGATG 1860
Db
1801 TGATTCATGTGTTGAAAAATGGAATGTAGATGTGCAAGGATTTGTTGTTCAAGAGATG 1860
QY
1861 TTCCGGAATTTATTTTATAGCAATTAAGAGTCAATCTGTTGGATGAGAGATGAGCTTTTA 1920
Db
1861 TTCCGGAATTTATTTTATAGCAATTAAGAGTCAATCTGTTGGATGAGAGATGAGCTTTTA 1920
QY
1921 AATGGCAAGCGCGCATGTAATAGCAATGTTTAACTCAAACTTTGGTTGGAACTAAATGAATA 1980
Db
1921 AATGGCAAGCGCGCATGTAATAGCAATGTTTAACTCAAACTTTGGTTGGAACTAAATGAATA 1980
QY
1981 GTATGTTGAGAAAGCTATATGCAAGAGATGCTTATGTCACCAATTTAAATGAATATA 2040
Db
1981 GTATGTTGAGAAAGCTATATGCAAGAGATGCTTATGTCACCAATTTAAATGAATATA 2040
QY
2041 TGGAAAAACGCTTACGTTGCTATTTGCAATTTAGGCCCGGATTTCTCAAGCCGCTATTTACTTTG 2100
Db
2041 TGGAAAAACGCTTACGTTGCTATTTGCAATTTAGGCCCGGATTTCTCAAGCCGCTATTTACTTTG 2100
QY
2101 TGGGGCCCAAAATTTATCAGAGGAGATGTTTGAAGCTCTGAATATCATAATCTATTTAAAGC 2160
Db
2101 TGGGGCCCAAAATTTATCAGAGGAGATGTTTGAAGCTCTGAATATCATAATCTATTTAAAGC 2160
QY
2161 TAATGAGCACGCGAGGTCGACTTTCTAAACGATATCCATAGCTTCAAGAGGGAATTTAAGG 2220
Db
2161 TAATGAGCACGCGAGGTCGACTTTCTAAACGATATCCATAGCTTCAAGAGGGAATTTAAGG 2220
QY
2221 AAGGCAAAATTAACCGCGTAGCATTTGCAATTTAGTAAACGAGAAAGTGGAAAGTGGAG 2280
Db
2221 AAGGCAAAATTAACCGCGTAGCATTTGCAATTTAGTAAACGAGAAAGTGGAAAGTGGAG 2280
QY
2281 AAGAGGTTCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
Db
2281 AAGAGGTTCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
QY
2341 TAATTTTGAAGAAAAATGTTAGCTTTCTTAGAGCTTTGAAGATGCAATTTTGAAGCA 2400
Db
2341 TAATTTTGAAGAAAAATGTTAGCTTTCTTAGAGCTTTGAAGATGCAATTTTGAAGCA 2400
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2401 TGTGTACGCTGTGAATTTTTTTTACGCAACGATCAGCGGTTTACTGGAACACCGATTC 2460
Db
2401 TGTGTACGCTGTGAATTTTTTTTACGCAACGATCAGCGGTTTACTGGAACACCGATTC 2460
QY
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Db
2461 TTGATACTCTGAGGACATCAATTTTCAACCCCGTTGGTCTTGTGATGAAATGAAGAAC 2520

QY	1640	TGCTAGGCAAAAGACCGCCTACTGTTATTTCTCTGTTGCTGCAACACTTTGTCCTCCGA	1699
DB	1966	TGCTAGGCAAAAGACCGCCTACTGTTATTTCTCTGTTGCTGCAACACTTTGTCCTCCGA	2025
QY	1700	ATTATCAGATGCGGTATTTTCATGGGCCAAAATGSCATATTAACACACAGTAGTTGATGA	1759
DB	2026	ATTATCAGATGCGGTATTTTCATGGGCCAAAATGSCATATTAACACAGTAGTTGATGA	2085
QY	1760	CTTTTTTGATATCGGTGGTCAATCGAATGGAATGACCAACCTGATTCATATGTTGGA	1819
DB	2086	CTTTTTTGATATCGGTGGTCAATCGAATGGAATGACCAACCTGATTCATATGTTGGA	2145
QY	1820	ATGGAATGATGTCGACAGGATGTTGTTGTCAGAGATGTTGCGATTTTATTTTACG	1879
DB	2146	ATGGAATGATGTCGACAGGATGTTGTTGTCAGAGATGTTGCGATTTTATTTTACG	2205
QY	1880	ATTAAAGATGCAATCTGTTGGATTGGAGTGAAGCTTTTAAATGCGACGCGCATGT	1939
DB	2206	ATTAAAGATGCAATCTGTTGGATTGGAGTGAAGCTTTTAAATGCGACGCGCATGT	2265
QY	1940	AACAGCCATGTTATTCAAACTTGGTTGGAACCTAATGAATAGTATGTTGAGAGAAGCTAT	1999
DB	2266	AACAGCCATGTTATTCAAACTTGGTTGGAACCTAATGAATAGTATGTTGAGAGAAGCTAT	2325
QY	2000	ATGGAACAGAGATGCTTATGTCACCAATTAATGAATATGGAACACGCTTACGTGTC	2059
DB	2326	ATGGAACAGAGATGCTTATGTCACCAATTAATGAATATGGAACACGCTTACGTGTC	2385
QY	2060	ATTTCATTTAGCCGATTTGTCAGCGGCTATTTACTTTTGGGGCCCAAAATTCACA	2119
DB	2386	ATTTCATTTAGCCGATTTGTCAGCGGCTATTTACTTTTGGGGCCCAAAATTCACA	2445
QY	2120	GGAGATGTTGTAAGCTCTGAATATCATATCTATTTAAGCTAAATGAGCACGCGGTCG	2179
DB	2446	GGAGATGTTGTAAGCTCTGAATATCATATCTATTTAAGCTAAATGAGCACGCGGTCG	2505
QY	2180	ACTTCTAAACGATATCCATAGCTTCAAGAGGGAATTTAAGGAAGGCAAAATTAACGCGGT	2239
DB	2506	ACTTCTAAACGATATCCATAGCTTCAAGAGGGAATTTAAGGAAGGCAAAATTAACGCGGT	2565
QY	2240	AGCATTTGATTTGAGTAAACGAGAAAGTGGAAAGTGGAAAGAGGTTGTGAGGAGAT	2299
DB	2566	AGCATTTGATTTGAGTAAACGAGAAAGTGGAAAGTGGAAAGAGGTTGTGAGGAGAT	2625
QY	2300	GATGATGATGATTAATAAACAAGAGGAAGAATTAATGAAATTAATTTTGAAGAAATGG	2359
DB	2626	GATGATGATGATTAATAAACAAGAGGAAGAATTAATGAAATTAATTTTGAAGAAATGG	2685
QY	2360	TAGCATTTGTTCTAGAGCTTTGAAGATGCAATTTTGGAAACATGTGTACAGTGTGAAATTT	2419
DB	2686	TAGCATTTGTTCTAGAGCTTTGAAGATGCAATTTTGGAAACATGTGTGTACAGTGTGAAATTT	2745
QY	2420	TTTTTACGCAACGATGACGGGTTTACTGGAACACGATTTCTTGATCTGTGAAGGACAT	2479
DB	2746	TTTTTACGCAACGATGACGGGTTTACTGGAACACGATTTCTTGATCTGTGAAGGACAT	2805
QY	2480	CATTTTACAAACCGGTTGGTCTGTGTAATGAAATGAAAGCAAAAGTAATTTGGCCTTTAA	2539
DB	2806	CATTTTACAAACCGGTTGGTCTGTGTAATGAAATGAAAGCAAAAGTAATTTGGCCTTTAA	2865
QY	2540	AAGATGATTAATATCATGCTCTTGAACGGGGTACTGTTGATGTTGTAATTAAGGTTT	2599
DB	2866	AAGATGATTAATATCATGCTCTTGAACGGGGTACTGTTGATGTTGTAATTAAGGTTT	2925
QY	2600	GTAGTTGATTAATAAGGTAATAGGTAATCAATAGAAAGCTTAAGTTTAAAGTTTTC	2659
DB	2926	GTAGTTGATTAATAAGGTAATAGGTAATCAATAGAAAGCTTAAGTTTAAAGTTTTC	2985
QY	2660	CTCGTGTACACACGCGTAGGTTCTTTGTTAAAGCAGTTTATTTATGTTTAGTACGACAC	2719
DB	2986	CTCGTGTACACACGCGTAGGTTCTTTGTTAAAGCAGTTTATTTATGTTTAGTACGACAC	3045

QY	2720	TTGGTGTTGTTGTTGTTGTTTATTTCTCTAAGAGCGTTTCACTTTGTTCTTAAAAAAA	2776
DB	3046	TTGGTGTTGTTGTTGTTGTTTATTTCTCTAAGAGCGTTTCACTTTGTTCTTAAAAAAA	3102
RESULT 3			
US-10-041-018-368			
; Sequence 368, Application US/10041018			
; Publication No. US2004007232A1			
; GENERAL INFORMATION:			
; APPLICANT: Matsuda, Seichi P. T.			
; APPLICANT: Hart, Elizabeth A.			
; TITLE OF INVENTION: Dicerene-Producing Unicellular Organism			
; FILE REFERENCE: P020800SI/10025547			
; CURRENT APPLICATION NUMBER: US/10/041,018			
; PRIOR FILING DATE: 2002-01-07			
; PRIOR APPLICATION NUMBER: US 60/259880			
; NUMBER OF SEQ ID NOS: 413			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 368			
; LENGTH: 2594			
; TYPE: DNA			
; ORGANISM: Lactuca sativa			
US-10-041-018-368			
Query Match 51.2%; Score 1428.6; DB 7; Length 2594;			
Best Local Similarity 75.8%; Pred. No. 0;			
Matches 1833; Conservative 0; Mismatches 529; Indels 57; Gaps 3;			
QY	238	CAGCTATTATCATACACATCAACTTCCATGTTGGGACAACTAATCCCACTAATCTGATCA	297
DB	187	CATCGGGTCTTCGTACAGCTTCTTCAACAGCTGGACAGTTAATCTCTATGATGACCC	246
QY	298	TTGATACAAACCAAGAACGATCCAAACACAGTTTAAACATCTAGAAATTTCTGTTTCTT	357
DB	247	TTGATGTGACCAAGAACGATCCGAAAGCTGTTCAACATGTGGAGTTTCTGTTTCTT	306
QY	358	CATATGACACAGATGGGTAGCCATGGTCCCTTCTCCAAACTCACCAATCGCTTGT	417
DB	307	CATATGACACAGTGGGTAGCCATGGTCCCTTCTCCAAACTCTCCCAATCCCTTGT	366
QY	418	TCCTTGAGTGTCTCAATTTGTTAAATTAATCAGCTTAATGATGTTTCATGCGGTCTTG	477
DB	367	TCCTTGATTTCTGAACTGGTTACTGGATAATCAGCTGATGTTTATGCGGTCT--	424
QY	478	TTAATCACACTCATATCATATCAATCACTCCGTTGCTTTAAAGATTCTCTATCTTCAACATTAG	537
DB	425	-----TCTTCTCATCAGTCCCATTAATTAAGATACTCTCTTCAACATTAG	474
QY	538	CATGTAATTTGCAATTAAGATGGAATGTTGGGGAAGATCAATTAATAAGGTCTAA	597
DB	475	CATGTGTAATTTGCAATTAAGATGGAATGTTGGGGAAGATCAATTAATAAGGTCTAA	534
QY	598	GTTTATTTAGTCAATCTTGTCTCAGCTACCTGAAAGAGTCAACCATCTCCATTTGTT	657
DB	535	ATTATTTAGTCAATTTTGTCTTCACTGACCAAAATCAAGCATCTCCATTTGGTT	594
QY	658	TTGACATCATATTTCTGTTTGTGTTAGTATGCGAAATACTTGGACATAAACCTCTTT	717
DB	595	TTGACATCATATTTCTGTTTGTGTTAGTATGCGAAATACTTGGACATAAACCTCTTT	654
QY	718	CAAAAACAAACAGATTTTGTGCTACATAAGAGGGAATTTGGAGCAAAAAGATGCC	777
DB	655	TAAACCAACACATTTGAGTGTGATTTACATGAGAGAGAAATTTGGAGCTTAAGAGATGC	714
QY	778	ATTCAAAATGAGATGATGATCTTGGCTATATCTCTGAAGACTCGGTAAATTTATATG	837
DB	715	ATTCAAAATGAGAGGAGATCTTGGCTATATCTCTGAAGACTCTGAAATTTTAAATG	774
QY	838	ATTGGAATATGTTGAAGAAATATCAGATGAAAAATGGTTCTGTTTTTCACTCAG	897
DB	775	ACTGGAACATGTTGATGAAATATCAAAATGAAGAATGGTTCTCTTTTCACTCAG	834

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QY 898 CAACAGCTGCTGCTTTCATTAATCATCAAAATCTGGTGTCTTAAATTTAAATTCAC 957
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 899 CAACAGCTTCTGTTCTTATTCATCATCAAAATGCTGGTGTCTTCAATTAACATTCAC 894
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 958 TTTTGGACAAGTTGGTAAATGCAAGTCCCAACAGTTTATCTCATGATTTATTTATCCGAC 1017
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 959 TCTTGGACAAGTTTGGAAATGCAAGTCCCAACAGTTTATCCCTATGATTATATATGTGAGGC 954
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1018 TTTCTATGTTGACACAAATGGAAGATTAGGAATTTTACACCAATTTTACAGAGTGGAAATTA 1077
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 955 TTTTCCATGGTTGACACACTTTGAAGATTGGGAATCAAAACGACATTTCAAGGTGGAAATCC 1014
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1078 AAAATGTTTTAGATGAAACATACAGATGTTGGGTGGAAACAGATGAGCAAAATATTCATGG 1137
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1015 AAAATGTTTTAGATGAAACATATAGATGTTGGGTGAGGGGATGTCAAATATTCATGG 1074
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1138 ATGTTGTAACATGCTGCTTTAGCTTTTCGGTTATTAAGGATCAATGGGTATGAAGTTTCCC 1197
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1075 ATGTTGTCACCTTGTCTTTAGCTTTTCGGGTA TTAAGAAGCAATGGGTATGAAGTCTCTT 1134
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1198 CAGATCCATTGGCTGAAATTAATAA-----TGAAATTAAGCTT 1233
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1135 CGATCCATTGGCTGAAATTAATAA-----TGAAATTAAGCTT 1194
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1234 TGAAGACGAAATATGCAAGCTTCTTGAACATATCATGCTGCACATATATATACCAAGAGG 1293
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1195 TCAAGACGTAATACATCTCTTGAAGTTTATAGGATCACAGATCATATATACAGAGG 1254
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1294 ATTTATCTTCTCGAAACAAATCTTGAAGTCAGCTGATTTTCTTCAAGAGATAATATCCA 1353
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1255 AGTTAGCTTTTACAGAAACAACTTGA-----CAAGTTATCTCC 1293
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1354 CTGATTCAAACAGGCTTCTTAAATTAATTCACAAAGAGTGGAAATGCTCTTAAGTTCC 1413
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1294 CTTCAAGATTAACAAGCTCTCTAAATATATCTTCAAGAGGTGGATGATGCTCTTAAGTTCC 1353
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1414 CTATCAATACCGGTTTGAAGCATTAACACATAGAGCAATATACAGCTTTTACAAATGTAG 1473
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1354 CCTTTAATGCGACCTAGAACGATGTCCTCACTAGAGAAACATAGAGCATTTACAAATTA 1413
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1474 ACAATCAAGAAATCTGAAACATACATATCACTCATCAAAATATTAAGTAAACACTGATTACC 1533
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1414 ACCATCAAGAAATCTTGAACATACATATAGCTCATCAAAACATTTAGCAACAAAGATTACC 1473
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1534 TAAGTTGCTGTTGAAGATTTCTACACCTGCCAATCTATTTATCGTGAAGAAATTAAG 1593
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1474 TAAAGTTAGCTGTGCAAGATTTCAATGAATGCCAATCTATCTATTTGTGAAGAACTAAAG 1533
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1594 GTCTTGAAGGTGGGTGAGAAATAAGTTGGACCAAGCTCAAGTTTGTAGGCAAAAGA 1653
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1534 ATCTTGAAGGTGGGTGAGAAACAGATTAAGCAAGCTCAAAATTTGTAGACAGAGA 1593
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1654 CCGCTACTGTTATTTCTGTTGCTGCAACACTTTGCTCCCGCAATATACAGATGCGC 1713
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1594 CAGCTACTGTTACTTTCTGCTGCTTCAATTTCTTCTCCCTGATTTATCAGATGCC 1653
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1714 GTATTTTCATGGGCAAAATATGCGATATTAATCAAGTAGTTGATGATTTTTTTGATACG 1773
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1654 GAATTTTCATGGGCAAAAGTAGCATCTCTACTACAGTAATGATGATTTTTTTGATGTTG 1713
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1774 GTGATCAATTCGATGATTAACCAACTGATTTCAATGCTGTTGAAGAAATGGAATGTAGATG 1833
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1714 GAGATCTATGGATGAACCTGGTGAACCTTTGTCATCATCATTTGAAATGGAATGTAAAGC 1773
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1834 TCGACAGGATGTTGTTTCAGAGCATGTTCCGATTTTTTATTTTATAGCAATTAAGAGATGCA 1893
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1774 TTGAAATGATGCTGTTTCAGAGGAGTTCGCTTTTATTTTATAGCACTTAAGATGCGAG 1833
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1894 TCTGTTGATTTGAGATGAAGCTTTTAAATGGCAAGCGCGCATGTAACATGAGCATGTTA 1953
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1834 TCTGTTGATTTGAGACAAAGCTTTTAAAGATTCAAGAACGCAATATATAACAAAGCATGTTA 1893
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 1954 TTCAAACTGTTTGGAACTAATGAATAGTATGTTGAGAGAAGCTATATGACAAAGAGATG 2013
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1894 TTGAATTTTGGTTGGATTTGGTGAAGATGTTTGGAGAGAGCTATATGCGCGAAAGATG 1953
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2014 CTTATGTGCCAACATTTAAATGAATATATGGAACCGCTTAAGTGTCTATTTGCAATAGGCC 2073
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1954 GTTCAATTTCCAAACATATAATGAATATATGGAATATGTTACGTTGTCTATTTGCTTTAGGCC 2013
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2074 CGATTTGCAAGCGGCTATTTTACTTTGTTGGGGCCCAAAATTTATCAGAGGAGATTTGTCAAA 2133
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2014 CGATTTGCTCTCTACTCTTTACTTTTGGGGTAAATTTGTGCGAGGAAGTTGTTTCAGA 2073
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2134 GCTCTGAATATCAATAATCTATTTAAGCTAATAGACGACGAGGCTCGACTTCTTAAACGATA 2193
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2074 GCTCCGAGTATCAACAGCTTTATGAGCTTATGAGCACTCAGGGTCTGCTCTCATGAATGATA 2133
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2194 TCCATAGCTTCAAGAGGGAATTTAAGGAAGGCAAAATTAACGCGGTAGCAATTTGCAATTTGA 2253
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2134 TCCATAGCTTCAAGAGGGAAGGAAGCGCGGGAATTTGAATGCTGTGGCAATTTGTACATGA 2193
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2254 GTAAACGGAAGTGGGAAGTGGGAAGAGGCTTGTGGAGGAGATGATGATGATTA 2313
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2194 GTATGGAAGAGTGGGAGTGTGGAAGAGAGGTTGTAGAGGAGATGAAGATTTTGACAA 2253
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2314 AAAACAGAGGAAGAAATTAATCAAAATTAATTTTGAAGAAAATGGTAGCATTTGTTCCCTA 2373
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2254 AAAGTCAAGGAAGAGATGATGAAATTTAGTTTGGAAACAAAGGAAGTTGTTGCCAA 2313
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2374 GAGCTTTGAAAGATGCAATTTTGAACATGTCACGCTGTTTGAATTTTTTACGCAAAACG 2433
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2314 GAGTATGCAAGAGATGATTTTGGAAATGTCATGTCGAATGTTGTAATCTTTTATGCGACAG 2373
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2434 ATGACGGGTTTACTGGAACACAGATTTCTTGATACTGTGAGGAGCATCATTTACACCGGT 2493
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2374 ATGACGGGTTTACTGGAATGCGCAATTTCTTGATGTTGTCGAAGAAATTTATATATGAACCTG 2433
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2494 TGGTGTCTTGTGAATGAAATGAAAGCAAAAGGTAATTTGGCTTTTAAAGATGATAATAAT 2553
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2434 TGTCCTCATGTTGATATATATCATTTGTTATACCAATTCGTATTATATTATAGCATTTCTC 2493
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2554 ATCATGCTCTTGACGGGGTACTGTTGTTAGTTGTTATATAAAGGTTGTAGTTGATATAA 2613
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2494 AAAAATGAACCAAGCATACTAGTATTTCTAGATCTCTAGTCTCTATTTATTTATTTT 2553
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2614 AAGGTAATAGTAAATCAAT 2632
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2554 AATATAGTTGTTAGCTAT 2572
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 4

US-10-041-018-367
; Sequence 367, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080051/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 367
; LENGTH: 2638
; TYPE: DNA
; ORGANISM: *Cucumis sativus*
US-10-041-018-367

Query Match 29.0%; Score 809.4; DB 7; Length 2638;
Best Local Similarity 62.0%; Pred. No. 1.8e-179;
Matches 1410; Conservative 0; Mismatches 811; Indels 54; Gaps 6;

Qy	267	GGTGGACAAACTAAATCCCACTAAATCTCTGATCATTTGATACAACCAAGAACGGATCCAAAAA	326
Db	159	GGCACAAAAACTAAAACTGGAGCTTTTCGGCTTTTTCGAAGAAACAAAAAGAAATAAAAAA	218
Qy	327	CAGTTTAAAAATGTAGAAAATTTCTGTCTTTCTTCATATGACACAGCATGGGTAGCCATGGTC	386
Db	219	TTGTTCAAAAATGTGTGAACCTTTCAATTTCTCGCATATGATATCTGCATGGGTGGCAATGGTC	278
Qy	387	CTTCTCCAAACTCACCCAAATCCCTTGTTTTCCTCGAGTGTCTCAATCTGGTTAAATTAAT	446
Db	279	CCTTCTCCAAACTCTCTTAATAAACCTCTTTTTCCTGAGTGCAATAAACTGGGTATTAGAT	338
Qy	447	AATCAGCTTAAATGATGGTTTATCGGGTCTTTGTTAAATCACATCATATAATACATACCOCG	506
Db	339	CATCAAAACCCGTATGGGTATGCGG-----CATCTCCATGACCATCAGTTG	396
Qy	507	TTGCTTAAAGATTCTCTATCTTCAACATTAGCATGTAATGTTGCATTTAAAAAGATGGAAT	566
Db	387	GTGATGAAGCCACTCTCTTATCCACATTAGCATGTGTTCTTACTCTCTAAAGCATGGGAT	446
Qy	567	GTTCGGGAAGATCAAAATAAATAAAGGTCTAAGTTTATTCAGTCAAAATCTTGCTTCAGCT	626
Db	447	ATCGGTGATGATCATATGAGCAAGCCCTTAGTTTATCAAGTCTAATATAGCTTCAGCT	506
Qy	627	ACTGAAAAAAGTCAACCATCTCCCATTTGGTTTGGACATCATATTTCTGTTGCTTTGAG	686
Db	507	ACTGATGAGAAATCAACGTTCTCTGTGGGATTTTGACATAATTTTCCCTGGTATGATTGAG	566
Qy	687	TATCGGAAAACCTTTGGACATAAACCTCTCTTCAAAACACACAGATTTTAGTTTGAATGCTA	746
Db	567	TATGCTAAAGACTTGAATTTGAATCTACCTTTGGCATCAATGAATGGGATGCTTTGGTT	626
Qy	747	CATAAGAGGGAATTTGGAGCAAAAAAGAT-----GCCATTTCAAATGAGATGGATGGATAC	800
Db	627	CAAAAGAAAGATTGGAGCTTAGAGCTGCTGTAGCAACTCTGAGGAGGAAAGCCAT	686
Qy	801	TTGGCGTATATCTCTGAAGGACTCGGTAAATTTATATGATTTGGATATPGGTGAAGAAATAT	860
Db	687	TTAGCGTATGTTTCAGAAGGAATTTGGAAAAATTTACAGGACTGGGAAATGGTCATGCGATAT	746
Qy	861	CAGATGAAAATGCTGCTGTTTTCACACTCACCAATCAGCAACAGCTGCTGCTTTTCATTAAT	920
Db	747	CAAAAGGAAGACGGATCACTGTTTAGTTCTCATCCACCGCAGTGGCTTTTATGCGAC	806
Qy	921	CATCAAAATCCTGTTGCTCTTAAATTTAAATTTCACTTTTGGACAAAGTTTGGTAATGCA	980
Db	807	AGAAATGATGATGCGCTGTTTAAATTAACCTTCGCTCAGTCTTTACAAAAGTTTCATAGTTCA	866
Qy	981	GTCCCAACAGHTTATCTCATGATTTATTTATCCGACTTTCTATGTTTGACACAAATTGAA	1040
Db	867	GTTCGCCCAATATATCTCTTGATATATATGCTCGTTTACACATGGTGTGATGCGCTTCAA	926
Qy	1041	AGATTAGGAATTTCCACACCATTTCAGAGTGGAAATTAATAATGTTTTAGATGAAACATAC	1100
Db	927	AAACTGGGATTTGATGGCCATTTCAAAGATGAGATTAGAGTGATTTAGATGAACATAC	986
Qy	1101	AGATGTTGGGTGGAAACGAGATGACCAATATTTCAATGGATGTGTAAACATGTGCTTTAGCC	1160
Db	987	AGCTGTTGGATGCAAGGGAGGAAAAATATTTCTAGATGCTTCAACTTTGTCGAATGGCC	1046
Qy	1161	TTTCGGTTATTAAGGATCAATGGGTATGAAGTTTCCCGATCCAGATCCAATTTGGCTGAATTACT	1220
Db	1047	TTCCGGATGTTACGTGTGTGAAGGATATGATGTTTCTTCAGATCAATTTGACTCAATTTCTCA	1106
Qy	1221	AA-----TGAAATTAGCTTTGAAAGACGAATATTCAGCTCTTTGAA	1259
Db	1107	GAAGGTCTCTTTTCAAAATTCCTCGGAGGACATTTAAAGACNTTTAGTGCTCTACTAGAG	1166
Qy	1260	ACATATCATGCGTCAACA---TATATATACCAAGAGGATTTATCTTCTGGAAACAAATC	1316
Db	1167	TTATTTAAGGCTCCCAAGATATCATTTATCCGATGAGTTTATTTCTCGAAAAATATAAAC	1226

Qy	1317	TTGAAGTCAGCTGATTTCTCTCAAAAGAGATAAATATCACTG-----ATTCAAAACAGG	13167
Db	1327	TCITGGACTAGTCGTTTCCTCGAATCATGGATTATCTAGTGGTTTCAGTTCAATCTGATAGA	12886
Qy	1368	CTTTCITAAATTAATTCACAAAGAGGTGGAAAATGCTCTTAAGTTCCCTATCAATACCGGT	14277
Db	1387	ACTGAGAGACTCGTGAACAAGAGGCGATTAAATGCTTTCCGAGTTCCCTTATTAATCAACT	13466
Qy	1428	TTGAACCGCATAAACACTAGACGGAATATACAGCTTTTCAAACTGACAAATACAAATACAAAT	1487
Db	1347	CTGGAACGCTTATCAATAAGCGAGCACTGGAAGTTACAGTGGAGACATGTTGAGGATT	1406
Qy	1488	CTGAAAACATATATCACTCATCAATATPAGTAAACACTGATTACTTAAGTTGGCTGTT	1547
Db	1407	TCAAAACAGCATATGCTCTTAAATTTTGGTCATCAAGATTTCITGGAACTTGCTGTGA	1466
Qy	1548	GAAGATTTCTACACCTGCCAATCTATTATTCGTGAAGAATTAAAGGCTCTTGAAGGTCG	1607
Db	1467	GAAGATTTCAATACCCCTGCAAGGCATACATCGCAAGGAACCTGAAGAGCTTGAANAATGG	1526
Qy	1608	GTGTTAGAGAAATAGTTGGACCACTCAAGTTTGTCTAGGCAAAAGACCGCTACTGTTAT	1667
Db	1527	GTCAATCGAANAATAATTTGGACAAGTTGAAATTTTCGAGACAGAAGTTAGGCTACTGCTAT	1586
Qy	1668	TTCTCTGTTGCTGCAACACCTTCGTCCTCCGAATATCAGATGCGGCTATTTTCATGGGCC	1727
Db	1587	TTTTTCTGCTGCAGCGACCTTAACCTCTCCAGAACTTTGTGATGCCCGCTTATCATGGCA	1646
Qy	1728	AAAAATGGCAATATTAATACTACAGTAGTTGATGACTTTTGTGATATTCGGTGGTACAAATCGAT	1787
Db	1647	AAAAATGGGCTACTCAACACCGTGGTTGATGATTTCTTTGATGTTGGAGGATCTGAAGAG	1706
Qy	1788	GAATTGACCAACCTGATTCAATCTGTTGAAAATGCAATGCTAGATCTGCAACAAGGATTGT	1847
Db	1707	GAATTGTTAAACCTTATACAAATTTGGTGGAAAAGTGGGATGCCAGTGGGGAACCGGTTAC	1766
Qy	1848	TGTTTCAGAGCATGTTCCGATTTTATTTTATAGCAATTAAGATGCAATCTGTTGGATTGGA	1907
Db	1767	TGTTTCCAAGGAGTTGAGATTATATTTCITTGCACTTCATAGCACAAATTTGTGAATAGGA	1826
Qy	1908	GATGAAGCTTTTAAATGGCAAGCGCGGATGTAACTAGCCATGTTATTCAAACTTGTTG	1967
Db	1827	AAAAAGCTTTTACCTTTGGCAAGGACGCGCTGATGAGGAAATGTTATCGATATTTTGGTTG	1886
Qy	1968	GAACTAATGAATAGTATGTTGAGAGAAGCTATATGCAACAAGAGATCCTTATGTGCCAAACA	2027
Db	1887	GCTTTGCTCCAGTCAATGAGGAAGGAAGCTGAAATGTTGAAAATTAAGGTAGTGCCTATCA	1946
Qy	2028	TTAAATGAATATATGGAANAACGCTTACGTGTCAATTTGCAATTAGSCCCGATTTGCAAGCCG	2087
Db	1947	TTGGAATCAGTACATGGAANAATGGCTATGTATCATTTTCTTTGGGACCTTATAGTCCCTTCCA	2006
Qy	2088	GCTATTTACTTTGTGGGGCCCAATTAATCAGAGGAGATTGTTGAAAAGCTCTGAAATATCAT	2147
Db	2007	ACGCTCTACTTTTGTGACCTTAAGCTTCCAGAGGAAAATTTGTTGGAATTTGTGAATACAAG	2066
Qy	2148	AATCTATTTTAAGCTATATGACACGCGGTGCACTTCTAAACGATATCCATAGCTTTCAAG	2207
Db	2067	AAGCTCTTTTAAGCTGATGAGCACTTCCTGGCCGCTTCTGAAATGATACTCGAACTTTTGAT	2126
Qy	2208	AGGGAAATTTTAAGGAAGCAAAATTAACCGCGGTAGCAATTGCAATTTGATGAACGAGAAAAGT	2267
Db	2127	AGAGGTCCAGCGNAAGGGAATTTAAATGCTTGTCTCTATACATGATTAGTGCCTGGT	2186
Qy	2268	GGGAAAGTGAAGAAGAGGTTGTGGAGGAGATGATGATGATGATTAATAAACAAGAGGAAA	2327
Db	2187	AAGCTCCACAAAGAGGAGGCCACTGAAGCAATGAAAGAGGAGATGTTGATAGGACGAGAAGA	2246
Qy	2328	GAATTAATGAATTAATTTTGAAGAAAATGGTAGCATTTGTTCTTAGAGCTTCTGAAGAT	2387
Db	2247	GAATCTGTTGAGATGATGTTTTTTCGAGGAGAACAGTACAA---TTCCAAGAGCTTGTGAAGAT	2303
Qy	2388	GCATTTTGGAAACATGTGTCACTGCTGTTGAAATTTTTTTTTTTCAGCAACAGATGACGGGTTTACT	2447

Db 2304 TTGTTCTGGAAGAGCTGCTGTTGTCATCTATTTTACAGGAAAGATGATGGTTTACA 2363
Qy 2448 GGAACACAGATTCTGATACCTGTAAGGACATCATTTACAAACCGTTGGTCTTG 2502
Db 2364 TCCATGAGTGTGTAAGTCTGCGAAAGCCTTATTTGAAACACCCATGGTTCTGG 2418

RESULT 5

US-10-041-018-378
; Sequence 378, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Mateuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 378
; LENGTH: 2658
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; FEATURE INFORMATION: Coding
; NAME/KEY: misc feature
; LOCATION: (1)-(2658)
; OTHER INFORMATION: Coding
US-10-041-018-378

Query Match 28.0%; Score 782.2; DB 7; Length 2658;
Best Local Similarity 61.3%; Pred. No. 4.5e-173;
Matches 1390; Conservative 0; Mismatches 823; Indels 54; Gaps 6;
Qy 275 AACTAATCCCACTAACTGATCATTTGATACCAACCAAGAACGGATCCAAAACAGTTTAA 334
Db 236 AACTAAAACCTGGAGCTTTCACATGATGATGATGATGATGATGATGATGATGATGAT 295
Qy 335 AAATGATGAAATTTCTGTTCTTTCATATGACACAGATGGTACCATGCTGCTCTCTCC 394
Db 296 CAAGGTGAACTTTTCACTTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 355
Qy 395 AAATCAACCAATCGCTTTGTTTCCCTGAGTGTCTCAATTTGGTTAAATTAATCAGCT 454
Db 356 AAATCTCTCAACCAACCTCTTTTCCCGAGTGTATAAATCTGGTATTAGATAGTCAACA 415
Qy 455 TAATGATGGTTCATGGGCTCTGTTTAATCACTCATATATCAATCAACCCGTTGCTTAA 514
Db 416 TGCTGATGGTTCATGGGGCTTACTCCACAACT-----GATCAGTTGCTGATGAA 463
Qy 515 AGATTCTCTATCTTCAACATTAGCATGATTTGTTGCAATTAAGATGGAATGCGGGA 574
Db 464 GGCAATCTCTTATCTACATTAGCATGTTCTTACTCTTAAAGGTTGGAATATTGGGCA 523
Qy 575 AGATCAATAAATAAAGGTCTAAGTTTATTTAGTCAAAATCTTGTCTTCACTACTGAAA 634
Db 524 TGATCATATGAGCAAGCCCTTGNATTTTATCAAGTCTAATATAGCTTCACTACTATGA 583
Qy 635 AAGTCAACCATCTCCCATTTGGTTTGGACATCATATTTCCCTGGTTTGGTTGAGTATGGAA 694
Db 584 GAACCAACGTTCTCCGTTGGGATTTGACATTTATTTTCCCTGGCATGATTGAGTATGCTAA 643
Qy 695 AACTTTGGACATAAACCCTCTTTCAAAACAAACAGATTTTATGTTGATGCTACATAAGAG 754
Db 644 AGACTTGAATTTGAATCTACCCCTTGGCACCGAAGCGTGGATGCTTGGTTTGGAAAGAA 703
Qy 755 GGAATTTGGAGCAAAAA-----AGATGCCAATTCAAATGAGATGGATGATTTGGCGTA 808

Db 704 AGAGTTGGAGCTGAGAAGCTGCAGAAAGCAACTCTGAAGGTGGAAAAGCCCTATTATTAGCGTA 763
Qy 809 TATCTCTGAAGGACTCGGTAATTTTATATGATTCGAATATGTTGTAAGAAATATCAGATGAA 868
Db 764 TGTTCAGAAAGGAATTTGAAAGTTTACAGGACTGGGATATGTTGATGCAATATCAAGAGAA 823
Qy 869 AAATGGTTCTGTTTTCAACTCACCATCAGCAACAGCTGCTTCTTCAATTAATCATCAAAA 928
Db 824 GAATGGATCACTGTTTAAATTTCTCCATCCACTACGGCAGCGCTTTTATGTCATAGAAATGA 883
Qy 929 TCCGTGTTGCTTAAATTTTAAATTTCACTTTTGGACAAGTTTGGTAAATCAGTCCCAAC 988
Db 884 TGATGGCTGTTTGTATCTTCGCTCACTCTTACAAAAGTTTGAATGGCTCAGTTCCAC 943
Qy 989 AGTTTATCCTCATGATTTATTTATCCGACTTTCTATGTTTGCACAAATTCGAAGATAGG 1048
Db 944 AATATATCTCTTGTATATATATCTCGATTACATGTTGTAGTACCTTCAAAAATTCGG 1003
Qy 1049 AATTTTCAACACCATTTTCCAGAGTGGAAATTTAAAAATGTTTTAGATGAAACATACAGATTTG 1108
Db 1004 AATTGCTCGGCATTTTCAAGAGGAGATTAGAAGCGTATTAGATGAAACTTTACAGGTCTTG 1063
Qy 1109 GGTGAAACGAGATGAGCAATATTTATGATGTTGTAACATGCTTTTACGCTTTTACGCTTTCGGTT 1168
Db 1064 GATGCAAGGAGAGGAAAAATATATTTCTAGATGCTTCAACTTGTGCAATGGCCTTTTCAAT 1123
Qy 1169 ATTAAGGATCAATGGGTATGAGTTTCCCGAGATCCATTTGGCTTGAATTAATACTAA----- 1222
Db 1124 GTTACGTTTGAAGGATATGATGTTTCTTCAGACCAGTTGACTCAATTTTTCAGAAATAT 1183
Qy 1223 -----TGAATTTAGCTTTTGAAGACGAATATGACAGCTCTTTCGAAACATATCA 1267
Db 1184 CTTTCCCAATTTGCTTTGGAGGATATTTTAAAGACTTTCGGTGCCTCGCTGGAGTTATATAA 1243
Qy 1268 TGGTCAATATATATATACAAAGAGGATTTATCTCTCT-----GGAACAAATCTTGAAGTC 1324
Db 1244 GGCCTCTCAGATTTATCAGCAGCCCGATGAATGTTCTTGGAAAAATATAAATCTCTTGGAC 1303
Qy 1325 AGCTGATTTCTTCAAGAGATATATCCACTGATTCAAACAGGCTTTCTAAA----- 1376
Db 1304 TAGTCTGTTTCTGAAGCATGGATTATCTAGTGAATTCAGTTTGTGATAGAACCGATAG 1363
Qy 1377 -TTAAATTCAAAGAGGTTGAAATGCTCTTAAAGTTTCCCTTATCAATCAATCCGTTTGAACG 1435
Db 1364 TGTGTTTAAACAGAGGCTGTTTAACTCTTGTAGTTTCCCTATATATGCAACTCTAGAACG 1423
Qy 1436 CATAAACACTAGACGAATATACAGCTTTTCAATGTAGACAAATACAAAGATTCGAAAAC 1495
Db 1424 CCTAATAAGTAAGAGGGCAATGGAAGTTTACAGTGGAGACATTTGTGAGGATTTTCAAAATC 1483
Qy 1496 TACATATCACTCATCAATATTTAGTAACTGATTACCTTAAGGTTGGCTGTTTGAAGATTT 1555
Db 1484 GCATATGCTGCTTAAATTTTGGCCATCAAGATTTTCTGGAACCTTGTCTGTAGAGGATTT 1543
Qy 1556 CTACACTGCAATCTATTTTATCTGTAAGAAATTTAAAGGTTTGAAGAGTGGGTGGTGA 1615
Db 1544 CATACCTTGCACAGCATTCATCTTAAAGAACTGGAAGAGCTTCAAGATGGGTGGTGA 1603
Qy 1616 GAATAAGTTGGACAGCTCAAGTTTCTAGGCAAAAGACGCGCTACTGTTTATTTCTCTGT 1675
Db 1604 AAACAAATTTGGACAGTTGAAATTTTTCAGACTGCACTAGGCTACTGCTTATTTTGTCTGC 1663
Qy 1676 TGCTGCAACACTTTTCTGCTCCGAAATATCAGATGGCGGTATTTTCATGGGCCAAAATGG 1735
Db 1664 GGACGAGCCCTTACTGATCTTCTGAACTTCAATGATGCTGCAATAGCATGGGCAAAAATGG 1723
Qy 1736 CATATTAACCTACAGTATGTTGATGACTTTTGTGATATCGGTGGTGTACATCGATGAATGAC 1795
Db 1724 TGTGCTCAGACCGTGGTTGATGATTTCTATGATGGTGGAGGATCTGAAGAGGAATGGA 1783
Qy 1796 CAACCTGATTTCAATGTTGAAAAATGGAATGTAGATGTGCAAGAGATTTGTTGTCAGA 1855
Db 1784 TAACCTTATAGAAATTTGGTGAAGAGTGGGATCTCTGATGGGAAAGTGGGTTTACTGTTTCCA 1843


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QY 1377 -TTAATTACAAAGAGGTGAAATGCTCTTAAGTTCCCTATCAATACCGGTTTAGAACG 1435
Db 1364 TGTGTTAAACAAGAGCTGTTAATGCTCTGAGTTCCCTTAATAGCAACTCTAGAACG 1423
QY 1436 CATAAACACTAGACGAAATATACAGCTTTTCAATGTAGACAATACAGAAATTCGAAAC 1495
Db 1424 CCTAATAAGTAAGAGGCAATGAAAGTTACAGTGGAGACATTTGTAGAGGATTTCAAAATC 1483
QY 1496 TACATATCACTCATCAATATTAGTACACTGTATTACCTTAAGGTTGGCTGTTGAAGATTT 1555
Db 1484 GCCATATGCTGCTTAATTTTGGCCATCAAGATTTTCTGGAACCTTGTCTAGAGGATTT 1543
QY 1556 CTACACCTGCAATCTATTATCTGTGAAGATTTAAAGGCTTTGAAGGTTGGGTGGGTAGA 1615
Db 1544 CATACCTCTCAAGCATTCTTAAGAACTTGAAGAGCTTCAAGATGGGTGGTTGA 1603
QY 1616 GAATAAGTTGACAGCTCAAGTTTGTAGGCAAAAGACCGCTACTGTTATTCTCTGT 1675
Db 1604 AAACAAATTGGACGAGTTGAAATTTTTCAGACTGCACCTAGGCTACTGCTATTTTGCTGC 1663
QY 1676 TGCTGCAACACTTTCTGCTCCGAATTTATCAGATGCGGCTATTTCATGGGCCCAAAATGG 1735
Db 1664 GGCAGCGACCTTACTGATCCTGAACCTTCATGATGCTGCGATAGCATGGGCACAAAATGG 1723
QY 1736 CATATTAACTACAGTAGTTGATGACTTTTGTGATATCGGTGGTACAAATCGATGAATGAC 1795
Db 1724 TGTGCTCACAGCGTGTGATGATTTCTATGATGTTGGAGGATCTGAAGAGGAATGGA 1783
QY 1796 CAACCTGATTCATATGTTGAAAATGGAATGTAGATGTGCAACAAGGATTTGTTTCAGA 1855
Db 1784 TAACCTTATAGATTTGTTGAAAGTGGATCTGATGGGGAAGTGGTTACTGTTCCAA 1843
QY 1856 GCATGTTGGAATTTATTTTATAGCATTTAAAGATGCAATCTGTTGGAATGGAGATGAAC 1915
Db 1844 GGACGTTGAGATTTGATTTCTTGCACTGCACAGCACAGTTTGTGAAATAGGAAGAAGC 1903
QY 1916 TTTTAAATGCAAGCGCGATGTAAGTACTAGCCATGTTTCAAACTTGTGTTGGAATTAAT 1975
Db 1904 TTTAGTATGGCAAGGACGAGTGTATGAGGAATGTTATCGATGGTTGGTGTGCTCTGCT 1963
QY 1976 GAATAGTATGTTGAGAGAACTATATGGAACAAGAGATGCTTATGTGCAACATTTAAATGA 2035
Db 1964 GAAGTGTATGAGAAAGAAAGCTGATGTTGTCGAACAATAGGTTAGTCCATCAATGGTGA 2023
QY 2036 ATATATGGAACCGTTACGTGCTATTTGCAATTTAGGCCGATTTGTCAAGCCGGCTATTTA 2095
Db 2024 ATATATGGAACAAGCCCATGTATCATTCGCGTTGGGACCTTATAATCCTTCCAATGCTCTT 2083
QY 2096 CTTTGTGGGCCCAAAATTAACAGAGGAGATTTGTAAGGCTCTGAATATCATATATCTATT 2155
Db 2084 CTTTGTGGGACCTTAACTCTCAGAGGAATGATTTGGAAGCTTGAATACCAAGAGTTATA 2143
QY 2156 TAAGCTAAATGAGCACGCGGTCGACTTCTTAAACGATATCCATAGCTTCAAGAGGGAAT 2215
Db 2144 TAAGCTGATGAGCACTGCTGCTGCTTAAGATGATATTGATCTTACATAGAGATG 2203
QY 2216 TAAGGAAGGCAATTAACCGCGTAGCATTTGCAATTTGAGTAAACGAGAAAGTGGGAAGT 2275
Db 2204 CAAAGAGGAAAGCTGAATTTCTGCTCTGTGATGATTTGATGGCGGTGTAATGTCAC 2263
QY 2276 GGAAGAAGAGGTTGTGGAGAGATGATGATGATTTTAAACACAGAGGAAAGAAATTAAT 2335
Db 2264 CAAAGAGAGGCCATTGAAGCAATTAAGGGGATTTTGAAGGCGCGATGAAGAGCTGCT 2323
QY 2336 GAAATTAATTTTGAAGAAATGTTAGCATTTGTTCTTAGAGCTTTGTAAGATGCTATTTG 2395
Db 2324 GGGGTAGTTTTCGAGAGAACTACAA---TTCCGAAGAGCTTTGAGGATTTGTTCTG 2380
QY 2396 GAACATGTGTACGTGTTGAATTTTATCGCAACGATGACGGGTTTATCGGAAACAC 2455
Db 2381 GAAATTTGATGCTCAATCTATTTTATACATGGAAGATGATGGGTACACTTCAAAATAG 2440
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QY 2456 GATTCTTGATCTGTGAAGGACATCATTTTACAACCCGTTGGTGTG 2502
Db 2441 GTTGTATGAACACTGTAAAGCCATGTTTGAACCCATCGATCTGG 2487
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RESULT 7

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US-10-041-018-377
; Sequence 377, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 377
; LENGTH: 2506
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-041-018-377
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Query Match 26.2%; Score 732.4; DB 7; Length 2506;
Best Local Similarity 59.8%; Pred. No. 2.3e-161;
Matches 1356; Conservative 0; Mismatches 876; Indels 48; Gaps 5;
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QY 270 GGACAACTAATCCCACTAATCTGATCATGATACCAACAAACGATCCAAAAACAG 329
Db 143 GTACAGCAAGAGCTAACATGTGAGCTTTGACCAACAAAGAGAGATTTAGGNAATG 202
QY 330 TTTAAAAATGTAGAAATTTCTGTTTCTTCATATGACACAGCATGGGTAGCATTCCT 389
Db 203 TTGGAGAAAGTGGAGCTTTCTGTTTGGCCTACGATAGTTGGGTAGCAATGGTTCCA 262
QY 390 TCTCCAACTCACCAATCGCTTGTTCCTGAGTGCTCAATTTGTTAAATTAAT 449
Db 263 TCACCAGCTCCCAAAATGCTCCACTTTTCCCAAGTGTGAAATGGTTATTGGATAAT 322
QY 450 CAGCTTAATGATGTTTCATGGGCTGTTGTTAAATCACACTCATATCATATACCCCTTG 509
Db 323 CAACATGAGATGATGATTTGGGACCTTGATACC-----ATGACCATCATCTCTT 373
QY 510 CTTTAAAGATTTCTATCTTTCAACATTTAGCATGTTATTTGTCATTAACAAAGATGGAAT 569
Db 374 AAGAAGGATGTTGTTATCATCTACACTGGCTAGTATCTCGCGTTAAGAAGTGGGAAT 433
QY 570 GGGAGAGATCAATTAATTAAGGCTTAAGTTTATTGAGTCAATCTTGTCTCAGCTACT 629
Db 434 GGTGAAGACAAATTAACAAAGGCTCTCCAGTTTATTGAGCTGAATTTCTGCAATTAGTCACT 493
QY 630 GAAAAAGTCAACCATCTCCCATTTGTTGACATCATATTTCTGTTTGTCTTGAGTAT 689
Db 494 GATGAAACCATACAGAAACCAAGGTTTGTATTTATTTCTGGGATGATTAATAT 553
QY 690 GCGAAAACTTGGACATAAACCTCTCTTTCAAAAACAAACAGATTTTGTGTTGATCTACAT 749
Db 554 GCTAGAGATTTGAATCTGACGATTTCCATTGGGCTCAGAAGTGGTGGATGATCATGATACGA 613
QY 750 AAGAGGGAATTTGAGCAAAAAAG-----ATGCCATTTCAATGATGATGGATGATAC 800
Db 614 AAAAGAGATCTGATCTTAAATGTGATGATGATAAGGTTTCAAAGGGAAGAGACATAT 673
QY 801 TTGGCGTATATCTCTGAAGGACTCGGTAAATTTATGATTGGAATATGTTGGTGAAGAAATAT 860
Db 674 CTGGCTATGTTTATAGGGGGAACAGAAACCTTAAGATTTGGGATTTGATAGTCAAAATAT 733
QY 861 CAGATGAAAAATGTTCTGTTTTCACCTCACTCAACAGCAGCTGCTGCTTTTCATTAAT 920
Db 734 CAAAGGAAAAATGGTCTGCTGTTTGTCTCCAGCCACACACAGCAGCTGCTTTTACTCAG 793
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Qy	444	AAATAATCAGCTTAATGATGGTTTCATGGGGTCT-TGTTAATCACACTCATATAATCATATATCA	502
Db	280	CAGAATCAGCAGGATGATGGATCTTGGGGTGTGACCCAATCTGACTCAT-----	328
Qy	503	CCCGTGTCTAAAGATTCTCTATCTTCAACAAATTAGCATGTATTCTTGTCATTAAAAAGATG	562
Db	329	--CGGTGAGCAGAGATGTTCTCCCTATCCAGTGTGCGATGTGTTCTTGGGTTGAAGAGATG	386
Qy	563	GAATGTTGGGGAAGATCAAAATAAAATAAGGTCTAAGTTTTATTTAGTGCAAAATCTTGCTTC	622
Db	387	GAATGTTGGCAGAGAGAACAATTTGGAGAGGACTGCAATTTTCATCGGAGGAATTTCTCTGT	446
Qy	623	AGCTACTGAAAAAAGTCAACCATCTCCCATTTGGTTTTTGGACATCATATTTCTCGTTTGGCT	682
Db	447	TGCTATGGACCAGCAGTTTCACTTCTCTATAGGTTTCAACATCACTCTTCTCGTTTGGCT	506
Qy	683	TGAGTATGCGAAAAAATCTTGGACATAAAACCTCTTTTCAAAAACAAACAGATTTTAGTTTGTAT	742
Db	507	TAACCTCGGCATTGATATGGGTTTAGAATTTCTGTATAAGACAACTGATGTCGTGGCAT	566
Qy	743	GCTACATAAGAGGGAATTTGGAGCAAAAAAAGATGCCA-----TTCAAAATGAGATGGA	793
Db	567	TCTTTCCCGCGGAGATGGAAATTTGAAAAAGGCTGGCTGTGATAGTTCTTTTGGAGAAA	626
Qy	794	TGGATCTTGGCGTATATCTCTGAAGACNCTGGTAATTTATATGATTTGGAATATGGTGAA	853
Db	627	AGCATATATGCTTTTATCCAGAAGAGATTGCGGAANTATGCTGGACTGGGATCAAGTTAT	686
Qy	854	GAATAATCAGATGAAAAATGGTTCGTGTTTTTCAACTCACCATTCAGCAACAGCTGCTGCTTT	913
Db	687	GAAGTTTCAGAGGAAGAATGGATCATTTGTCAGCACCTCTTCCACAACCTGCTGTGCAAT	746
Qy	914	CATTAAATCATAAATCCTGGTGTCTTAATTAATTTAAATTCATCTTTTGGACAAGTTTGG	973
Db	747	AATCCAAAAATACAAACGACCAAGCCCTTCAATACCTAAATTTGCTTCTCAGTGCAATTTGG	806
Qy	974	TAATGCAGTCCCAACAGTTTATCCTCATGATTTATTTATCCGACTTCTATGTTGGTGACAC	1033
Db	807	CAGTGCAGTACAGCAATGATCTCTCAATGGGTACAATGTCAGCTTTTCAATGGTGGACGC	866
Qy	1034	AAATTGAAAGATTAGGAAATTTCAACACCAATTTCAGAGTGGAAATTTAAAAATGTTTTAGATGA	1093
Db	867	GCITGAAAAAATGGGAATTTCTCAGCGCTTTGTCAAGTGAATAGAAAGCATCTGGACAT	926
Qy	1094	AACATACAGATGTTGGTGGAAACGAGATGAGCAAAATATCATGGAATGTTGTAAACATGTGC	1153
Db	927	GGCATACAATTGCTGGTTTACAGAAAGATGAGGAAATCATGATGACATAGCAACATGTGC	986
Qy	1154	TTTTAGCCTTTCCGTTATTAGGATCAATGGGTATGAAATTTTCCCCAGATCCATTTGGCTGA	1213
Db	987	AATGGCAATTTCCGCTTTTGAGGATGAATGGTTTACATGTTTCTCCAGATGAGCTGTCTCA	1046
Qy	1214	AAATTACTAATG-----AAATTAGCTTTGAAAGACGAATATGC	1249
Db	1047	CGTTGCTGGAGCTTCCACTTTCCATGATTCACATCAAGGATATTTAATGATACAAATC	1106
Qy	1250	AGCTCTTGAACACATATCATGGGTACATATATTTATACCAAGAGATTTATCTTCTCGAAA	1309
Db	1107	CCTACTGGAATTTGTACAAGACCTCAAAGTCACTTATTCAGAAAAACGATCTGATCTTAGA	1166
Qy	1310	ACAAATCTTGAAGTCAGCTGATTTTCTCAAAGAGATAATCCCACTGATTTCAAACAGGCT	1369
Db	1167	TGCAATAGGTTCTGGTCTGGCAATTTATTGAAGGATAAGATGCTGTAGTAGGGTGCA	1226
Qy	1370	TTCTTAAATTAATTCACAAAGAGGTGGAAAAATGCTCTTTAAGTTTCCCTATCAATACCGGTTT	1429
Db	1227	AAAAGACTCGATTTTTCGAGAGATGGAGTATGCTGTGTTAAATTTTCCCTTGTATTCCCACT	1286
Qy	1430	AGAACGATTAACACTAGACAAATATACAGCTTTTACATGTAGACAATACAGAAATTTCT	1489
Db	1287	GGAGCGTCTAGAACACAAGAGAAACATTCGAACATTTTGAATGCTTTGGGGTCTCTGATGCT	1346

RESULT 9

RESOL 3
US-10-425-115-22041

US-10-423-113-22041 : Sequence 22041, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

```

; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 22041
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_120098C.1
; US-10-425-115-22041

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Query Match	20.0%;	Score 559.6;	DB 8;	Length 2716;
Best Local Similarity	56.1%;	Pred. No. 1.1e-120;		
Matches 1209;	Conservative 0;	Mismatches 894;	Indels 53;	Gaps 6;
QY	324	AAACAGTTTTAAATAATGTAGAAAATTTCTGTTCTTCATATGACACAGCATGGGTAGCCATG 383		
DB	234	AATCAGCTCCGGAAGCCCCAGTTGCCACCTTCTTCATACGACACAGCGTGGGTTCTTAG 293		
QY	384	GTCCCTTCTCCAAATCACCACAAATCCGCTTGTGTTCCCTCAGTGTCTCAATTTGGTTAATT 443		
DB	294	GTCCAGTGGGGCTCTCATCAGACTCCCGCTTCCACAGTGTGTGAGTGGATATTG 353		
QY	444	AATTAATCAGCTTAATGATGGTTCAATGGGGTCT-TGTTTAATCACACTCATTAATCAATATCA 502		
DB	354	CAGAAATCAGCAGGATGATGGATCTCTGGGGGTGTGAGCCAATCTGACTCAT----- 402		
QY	503	CCCGTTGCTTTAAAGATTCTCTATCTTCAACAATAGCATGTATTGCTTCATTTAAAAAGATG 562		
DB	403	--CGGTGAGCAAGGATGTTCTTCCTATCCAGTTGGCATGTGTTCTTCGTTGAAGAGATG 460		
QY	563	GAATGTTGGGGAAGATCAAAATAAAAGGCTTAAAGTTTATTGAGTCAAAATCTTGCTTC 622		
DB	461	GAATGTTGGCAGAGAGAACAATTTGGAGAGACTGCAATTCATCGGAGGAATTTCTCTGT 520		
QY	623	AGCTACTGAAAAAGTCAACGATCTCCATTTGGTTTGGACATCATATTTCTCTGTTTGCT 682		
DB	521	TGCTATGGACCGCAGCTTCACTTCTCCTATAGGTTTCAACATCACCTTTCTCGTGTGCT 580		
QY	683	TGAGTATGCCGAAAACCTTTGGACATAAACCTCTTTTCAAAAACAAACAGATTTTACGTTTGAT 742		
DB	581	TAACTCGGCATTGATATGGGTTTAGAATTTCTGTGAAGACAAACTGATGCTGTGGCAT 640		
QY	743	GCTACATAAGAGGGAAATGGGAGCAAAAAAGATGCCA-----TTCAAAATGAGATGGA 793		
DB	641	TCCTTCCGCGCGGAGATGGAAATTTGAAAAGCTGGCTGGGATAGTTCTTTTGGAGAAA 700		
QY	794	TGGATCTTGGCGTATATCTCTGAAGAGACTCGGTAAATTTATATGATTTGGAATATGGTGAA 853		
DB	701	AGCATATATGGCTTTTATCCAGAAGGATTCGGAAATAATGCTGACCTGGGATCAAGTTAT 760		
QY	854	GAATAATCAGATGAAAATGGTCTGTTTCAACTCACCATCAGCAACAGCTGCTGCTTT 913		
DB	761	GAAGTTTCAGAGGAAGAAATGGAATCATTTTCAGCACTCCTTCCAACTGCTGTGTGAAAT 820		
QY	914	CATTAAATCATCAAAATCCTGGTGTCTTAAATTAATTTAAATTTCACTTTTGGACAAGTTTGG 973		
DB	821	AATCCACAAATACAAACCAAGCCCTTCAATACCTAAAATTTGCTTGTTCAGTGAATTTGG 880		
QY	974	TAAATGAGTCCAAACAGTTTATCCTCATGATTTATTTATCCGACTTTCTATGTTGTGACAC 1033		
DB	881	CAGTGCAGTACACAGCAATGTATCCTTCAATGGGTACATTTGTTCAGCTTTCAATGGTGGACG 940		
QY	1034	AATTTGAAGATTAGGAATTTTACACACCATTTTCAGAGTGGAAATTAATAATGTTTTAGATGA 1093		
DB	941	GCTTTGAAAAAATGGGAATTTTCTCAGCGCTTGTTCAGTGAATAGAAAGCATCTCTGGACAT 1000		
QY	1094	AACATACAGATGTTTGGGTGGAAACGAGATGAGCAAAATATTCTATGGAATGTTGTAACATGTC 1153		

D	b	1001	GGCATAAAATTGCTGGTTACAGAAAGATGAGGAATCATGTGCATATGCAACAATGTCG	1067
Q	y	1154	TTTAGCGCTTTCGGTTATTAAAGGATCAATGGGTATGAAGTTTTCCCGAGATCCAATTGGCTGA	1213
D	b	1061	AATGGCATTTGGCTTTTGAGGATGAATGGTTACAATGTTTTTCCTCAGATGAGCTGCTCA	1120
Q	y	1214	AATTACTAATG-----AATTAGCTTTTGAAGACGAATATGC	1249
D	b	1121	CGTTGCTGGAGCTTCCACTTTTCCATGATTCACATCAAGGATATTTAAATGATACAAAATC	1180
Q	y	1250	AGCTCTTGGAAACATATCATCGCTCACATATTTATACCAGAGGATTTATCTTCTCGAAA	1309
D	b	1181	CCTACTGGAAATGTCAGAAGCTCAAAGTCACCTTATCAGAAAAAGATCTGATCTTAGA	1240
Q	y	1310	ACAAATCTTGAAGTCAAGCTGATTTCTCTCAAAGAGATAATCCACTGATTTCAAACAGGCT	1369
D	b	1241	TCCATAGGTTCTGGTCTGGCACTTATTGAAGGATAAGATGCTGCTAGTAGGGTGCA	1300
Q	y	1370	TTCTAAATTAAATTCACAAAGAGGTGGAAATATGCTCTTAAGTTTCCCTATCAATACCGGTTT	1429
D	b	1301	AAAAGACTCGATTTTTCGAGAGATGAGTATGCTGTAAATTTTCCCCTGTGATTTCCACACT	1360
Q	y	1430	AGAACGCTAACAACACTTAGACGAATATACAGCTTTTACAATGTATAGACAATAACAAGAAATCT	1489
D	b	1361	GGAGCGTCTAGAACACAAGAGAAACATCGAACATTTTGATGCTTGGGGTTCTCTGATGCT	1420
Q	y	1490	GAAAACTACATATCACTCATCAAAATATTAGTAACTGATTAAGGTTTGGCTGTGTTGA	1549
D	b	1421	--AACAAACAAATCTCATCTTTTCGTATCAATCAAGAAATTCCTAGCTTTGGCAGTCGA	1477
Q	y	1550	AGATTTCTACACTGCCAAATCTTATTTATCGTGAAGAAATTTAAAGGTTCTGAAAAGGTGGGT	1609
D	b	1478	AGATTTCAAGTTTCTCTCAACGCTTTTCCGGGATGAACCTTCGGCATCTTGATAGTTGGGT	1537
Q	y	1610	GGTAGAGATAAGTTGGAACGAGCTCAAGTTTGTGTAGCAAAAAGACCGCTACTGTTATTT	1669
D	b	1538	GAAGGAGAACAGCTGGACGAGCTACAAATTTGTCTCGGCAGAAACTGACATATTGCTATCT	1597
Q	y	1670	CTCTGTTGCTGCAACACTTTTCGCTCCCGAAATTTACAGATCGCGTATTTTCATGGGCGAA	1729
D	b	1598	GTCTGCTGCTGCTPACCGTATTTTCTGNAATTTGTGACGCTCGCANTTTCATGGGCGAA	1657
Q	y	1730	AAATGGCATATTAACTACAGTAGTTGATGACTTTTTTTTGATATCGGTGGTACAATCGATGA	1789
D	b	1658	AAATGGTGCTCTCACAACTGTGGTTGATGACTTTTCGATGTTGGTGGATCAAAAAGAAGA	1717
Q	y	1790	ATTGACCAACTGATTCATGTTCTGNAANAATCGAATGTAGATGTGCACAAGGATTTGTTG	1849
D	b	1718	ATTAGAAAACCTGATAGCACTAGTTGAGAAATGGCATGGCCACCATGCGAGTTGATTCCTA	1777
Q	y	1850	TTCAGAGCATGTTTCGGATTTTATTTTGTAGCATTTAAAGATGCAATCTGTTGGATTTGAGA	1909
D	b	1778	TTCCGAACAGTGAANAATAGTATTTTCTGCTATTTATACAACAGTGAACCATCTTGGAGC	1837
Q	y	1910	TGAAGCTTTTAAATGGCAAGCGCGGATGTAATCTAGCCATGTTTATTCAAACTGTTGGGA	1969
D	b	1838	AATGGCTTCTCGAGCAACAAGCGCTGATCTTACAACCACTAGTAGAANAATATGGCTTGA	1897
Q	y	1970	ACTAATGAATAGTATGTTTGAGAGAGCTATATGGAACAGAGATGCTTATGTCGCCACATTT	2029
D	b	1898	TTTGTTTAAGATCTATGATGGTCGAGCGCAATGGCAGAGATGCCAATATGTACCAACAGT	1957
Q	y	2030	AAATGAATATATGAAAAACCTTTACGTGTCATTTTGATTAAGSCCGGATTTGTCAAGCCGGC	2089
D	b	1958	TGAAGAATACATGACAAATGCTGTTGCTCATTTTGTGNCTGGGCCCAATTTGCTCCCCAGC	2017
Q	y	2090	TATTTACTTTTGTGGGGCCCCAAATATATCAGAGGAGATTGTTGAAAGCTCTGAAATATCATAA	2149
D	b	2018	ATTGTAATTTTGTAGGGCAAGAGCTATTAGAGCATGCTGTCAAAGA TGAAGAGTACGATAA	2077
Q	y	2150	TCTATTTTMACTAATGAGCAACGAGGTGCACTTCTTAAACGATATCCATAGCTTCAAGAG	2209
D	b	2078	ATTATTTAGGCTAGTGAGCACTTCGCGGAGGGCTCCTCAATGACTTCAAGATTTTAGAG	2137


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1073 CTGCGTGTGATGTCGCAAAAGCATCATGCTCAGCGTGTAGTGTGACTTCTTCGATG 1132
1771 TCGGTGTGATCAATCGATGATGACCACTGATTCATGTTGTTGAAGATGATGATG 1830
1133 TTGGTGTGATCAAAAGAAAGAACAAAGAAATCTCATCGAAATAGTGTGAGAACTGGGATGAGC 1192
1831 ATGTGCAAGAGGATGTTGTTTCAGAGCATGTTTCGATTTTATTTTATAGCAATTAAGATG 1890
1193 ACCACAAAGTTGATCTGTTTCGGAGAAAGTAGAAATAGTTTCTATGCTGTCTATAATA 1252
1891 CAATCTGTTGGATGGAGATGAAGCTTTTAAATGGCAAGCGCGGATGTTAACTAGCCATG 1950
1253 CAGTGAACCAAGCTTGTGATCTATGCTTCTGAGTACAGAAAGCGGATGTTGACAAAACACC 1312
1951 TTATTCAAACTGTTGGAACTAATGAATAGTATGTTGAGAGAGCTATATGACAGAG 2010
1313 TCGTGAACCATGGCTTAAAGTATGCTGTGCAATGCTGACGAGGAGAGCTTGGCAAGGA 1372
2011 ATGCTTATGTGCCAACATTAATGAATATATATGAAAACGCTTACGTGTCAATTTGCAATTAG 2070
1373 GGCAATTTGTACCAACAGTTGAGGAATAACATGCAAAATGAGTTTCTTCTTGGCACTGG 1432
2071 GCCCGATGTCAAGCCGGCTATTATCTTTGTGGGCCCCAAATATATACAGAGGAGATTGTTG 2130
1433 CGGTCAATTATCTCCAGCGCAGTATTTTCTTGGCGAAACGCTCTCAGATTACATGCTCA 1492
2131 AAAGCTCTGAATATCATATTAATTAAGCTAATATGACGACGCGAGGCTCGACTTCTAAACG 2190
1493 AAGATCATGAATACAGCAATTTTGTCTGAGCTCATGTTTCACTTGCAGTCGCTCTTAAATG 1552
2191 ATATCCATAGCTTCAAGAGGGAATTTAAGGAAGCAAAATTAACGCGGTAGCATTTGCATT 2250
1553 ACATTGCAAGCGTTGAGAGGAGTTTCCAGCTGGTAAATCTGAACAGCGTTTCACTGCTTG 1612
2251 TGAGTAAACGAGAAAGTGGGAAAGTGGAAAGAGAGTGTGGAGGAGATGATGATGA 2310
1613 CTCTACACAGTGTGGTTCATGTCCATAGAGCGGCTAAGAGGAAACACATGGATCTT 1672
2311 TTAAGAACAGAGAAAGAAATTAATGAATTAATTTTGAAGAAATGGTAGCATTTGTTTC 2370
1673 TAGAGTGTATAGGAGAGGTTTAGTACGCTTGGTTCGT---AGACAGGACAGTGTGTTTC 1729
2371 CTAGAGCTCTTAAAGATGCAATTTTGAACATGTGTACGCTGTGAATTTTTTTTACGCAA 2430
1730 CTAGGTCAATCAAGAGCTGTTCTGGAAGCTTTTGGAAAGCTTTTGGAAAGCAATTCACCTGTTCTACTTC 1789
2431 ACAGTACGCGGTTTAC 2446
1790 AGATTGATGATTTAC 1805

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RESULT 12

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US-10-425-115-175619
; Sequence 175619, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 39-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 175619
; LENGTH: 2364
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_91756C.1

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US-10-425-115-175619
Query Match      15.4%; Score 430; DB 8; Length 2364;
Best Local Similarity 55.7%; Pred. No. 3.4e-90;
Matches 945; Conservative 0; Mismatches 715; Indels 36; Gaps 5;

QY 778 ATTCAAAATGAGATGGATGATGATGCTGCGGTATATCTCTGAAGGACTCGGTAATTTATG 837
DB 120 AATCTACGCAATAGAGCATATTTGCGCTATGTTCTGAAGGTTCCGAAACCTGCTGG 179
QY 838 ATTGGAATATGGTGAAGAAATATCAGATGAAGAAATGTTCTGTTTCACTCACTCAATCA 897
DB 180 ACTGGAATATGATGTTATGAAGTTCCAAAGCGAAGATGATCCTTTGTTAACTCTCTCTG 239
QY 898 CAACAGCTGCTGTTTCAATTAATCATCAAAATCCTGTTGCTTAAATTTTAAATTCAC 957
DB 240 CAATCTGCTGCGCTTTGTCGCGCACTATGACGAAAGCGGTACAGTATCTAAATTTGC 299
QY 958 TTTTGGAACAAGTTTGGTAAATGTCAGTCCCAACAGTTTATCTCTATGATTTATTTATCCGAC 1017
DB 300 TTGTCACACAAATTTGGCAGTGTCAGTACCAACAGTGTCCACACAAATATTTCACTATCAGC 359
QY 1018 TTTCTATGTTGACACAAATTTGAAGATTTAGGAATTTACACCAATTTTCAAGATGAGAAATTA 1077
DB 360 TTTCAATGTTGGACACGCTCGAAAGTTTGGAAATATCAGGCATTTTCTGTGGAGAAA 419
QY 1078 AAAATGTTTGTAGATGAACATACAGATGTTGGGTGGAACGAGATGAGCAATATTCATGG 1137
DB 420 AGCTGTCTGGACATGATATACAGTTTGTGGTTACAGAAAGAGGAGGAAATATGTTGG 479
QY 1138 ATGTTGTAACATGCTGCTTTAGCCTTTTCGGTTTATTAAGGATCAATGGGTATGAAGTTTCCC 1197
DB 480 ATGCAAGACATGTCGATGGCAATTTTCAATTTTCAAAATGATGCTTTGATGTTTCCA 539
QY 1198 CAGATCCATTTGGCTGAAATTTAATAATG-----AATAGCTT 1233
DB 540 CAGATTTGGTTGTTCTCATATTTGCTGAAGCCTCCAATTTTCCATACTCACTACAAGGATTT 599
QY 1234 TGAAGACGAAATATGACGCTCTTTGAACATATCATCGCTC---ACATATATTTATACCAAG 1290
DB 600 TATGTATCAAAAGATCTTATTTGGAATATGTAACAAAGCCTTAAAGTCATATATTCAGAAA 659
QY 1291 AGATTTATCTTCTGAAAAACAAATCTTGAAGTTCAGTGTATTTCTTCAAGAGATATAT 1350
DB 660 GAGACTTTGACTTAGAGACATAGGATGTTGACAGGTAGCTTATTCAGCGGAAAGCTAT 719
QY 1351 CCACTGATTCAAACAGGCTTTCTAAATTAATTCACAAAGGTTGGAAGATGCTCTTAAGT 1410
DB 720 GCTCTGATGGA---GCGCAAGAGATACCGATCTTGAAGAGGTAGAGTATGCCCTTAAAGT 776
QY 1411 TCCCTATCAATACCGGTTTAGAACGCTAAGACACTAGACGAAATATACAGCTTTACAGT 1470
DB 777 TTCCCCCATTTAGCCGTAGTAGATCTCTCAACAAACAGAAAGATATGAGGATTTGGATG 836
QY 1471 TAGACAAATCAAGAAATTTCTGAAAACTACATATCACTCATCAAAATATTTAGTAACCTGATT 1530
DB 837 CTAGGGGTTCTCAGAGCTTAAGACAAATATCTGCCATGTCTATGATGAAGTCA---AGACA 893
QY 1531 ACCTAAGGTTGGCTGTTGAAGATTTCTACCTGCCAAATCTATTTATTCGTGAAGAAATTA 1590
DB 894 TCCTTGGTGGCTGTTGAAGATTTCTGTTTCTCAATCTATTTTCCAGGAGGAACTAC 953
QY 1591 AAGGCTTTGAAAGGTTGGTGAAGAAATGTTGGACGAGCTCAAGTTGCTTAGGCAAA 1650
DB 954 AGAACATCAATTTAGTTGGGAGAAAGAGATAGGATGAGCAGCTACAAATTTTGTGCGGAAA 1013
QY 1651 AGACCGCTTACTGTTATTTCTGTTGCTGCAACACTTTTCTGCTCCCGAATTTATCAGATG 1710
DB 1014 GGCTGCAATATTTGCTATCTCGCTGCTGCTACCAACATATCCCCCTCATGATTTCTGATG 1073
QY 1711 CGCGTATTTTATGCGGCAAAATATGCGATATTAATCACTAGTGTGATGACTTTTTTTGATA 1770
DB 1074 CTGCGGTTGATGTCGCAAAAGCATCATGCTCAGGTTGTAGTTGATGACTTCTTCGATG 1133

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QY 1771 TCGGTGGTACAAATCGATGAATTGACCAACCTGATTCATATGTGTTGAAAAATGGAATGTAG 1830
Db 1134 TTGGTGGATCAAAAGGAACAAGAAAATCTCATCGAATTTAGTTGAGAACTGGGATGAGC 1193
QY 1831 ATGTCCACAAGGATTTGTTGTCAGAGCATGTTCCGGATTTTATTTTAGCATTAAGAGATG 1890
Db 1194 ACCAAGAAGTTGATTTCTGTTCCGAGAAAGTAGAAATAGTTTCTATGCTGCTATAATA 1253
QY 1891 CAATCTGTTGGATTTGGAGATGAAGCTTTTAAATGGCAAGCGCGCATGTAACCTAGCCATG 1950
Db 1254 CAGTGAACAGCTTTGATCTATGCTTCTGCACTACAGAAGCGCGATGTGACAAACACC 1313
QY 1951 TTATTCAAACTGGTTGGAACTAATGAATAGTATGTTGAGAGAGCTATATGGAAGAAG 2010
Db 1314 TCGCTGAATCATGGCTTAAAGTATTTCTGTGCACTGCTGACGAGGAGAGCTGGCAAGGA 1373
QY 2011 ATGCTTATGTGCCAACATTAAATGAATATATGAAAAACGCTTACGTTGTCATTTGCAATTAG 2070
Db 1374 GGCAATTTGTACCAAGTTGAGGAATACATGGCAATGCAAGTTTCTCTTGGCACTGG 1433
QY 2071 GCCCGATTTGCAAGCGCGCTATTACTTTGTTGGGGCCCAAAATTTATCAGAGGAGATTTGTTG 2130
Db 1434 CGGTCAATATATCTCCAGCGCAGTATTTTCTTGGCGAAACGCTCTCAGATTACATGTTCA 1493
QY 2131 AAAGCTCTGAATATCATATATCTATTTAAGCTAATGAGAGCGCAGGCTGACATTTCTAAACG 2190
Db 1494 AAGATCATGAATACAGCAATTTGCTGAGCTCATGTTCTACTTGCAGTCGCTCTCTTAAATG 1553
QY 2191 ATATCATAGCTTCAAGAGGGAATTTAAGGAAGGCAAAATTAACGCGGTAGCATTCATTT 2250
Db 1554 ACATTCGAAGCGTTGAGAGGGAGTTTGAAGCTGTTGAATCTGAACAGCGTTTCACTGCTTG 1613
QY 2251 TGAGTTAACCGAGAAAGCTGGGAAAGTGGGAAGAGAGGTTGTGGAGGAGATGATGATGATGA 2310
Db 1614 CTCTACACAGTGGTGTTCATGTCCATAGAGCGGCTAAGAGGAAACACATGGATCTT 1673
QY 2311 TTAAAAACAGAGGAAAGAAATTAATGAATTAATTTTGAAGAAATTTGAGCAATTTGTTTC 2370
Db 1674 TAGAGTCTGATAGGAGAGGTTTAGTAGCGTTGGTTCTGTT---AGACAGGACAGTGTGTTTC 1730
QY 2371 CTAGAGCTGTTAAGATGCAATTTTGAACATGTTGACAGTGTGTAATTTTGTAGCAAA 2430
Db 1731 CTAGGTCTGCAAGGAGCTGTTCTGGAAGCTTTTGAAGCAATTCACCTGTTCTACTTCC 1790
QY 2431 ACAGTACCGGTTTAC 2446
Db 1791 AGATTGATGAATTTAC 1806
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RESULT 13
US-10-425-114-5988
; Sequence 5988, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5988
; LENGTH: 2029
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700550363_FLI
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US-10-425-114-5988

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Query Match 14.1%; Score 392.4; DB 7; Length 2029;
Best Local Similarity 53.9%; Pred. No. 2.3e-81;
Matches 999; Conservative 0; Mismatches 741; Indels 112; Gaps 5;

QY 700 TGGACATAAACCTCCTTTCCAAAACAAACAGATTTTAGTTTGTATGCTTACATAAGAGGGAAT 759
Db 4 TGGGTTTAGAATTTCTCTGTAAGACAAACCTGATGTCGTGGCAATCTTCCACCGCGGAG 63
QY 760 TGGAGCAAAAAAG-----ATGCCATTCAAATGAGATGGATGGATGATCTTGGCGTATA 810
Db 64 TGGAAATTGAAAGCGCTGGCTGTGGATAGTTCTTTTGGAGAAGACATATATGGCTTTTA 123
QY 811 TCTCTGAAGGACTCGGTAAATTTATATGATGGAATATGTTGGAAGAAATATTCAGATGAAAA 870
Db 124 TCCAGAAGGATTCGGAATATATGCTGCACTGGGATCAAGTTATGAAAGTTTCAGAGGAAGA 183
QY 871 ATGGTTCTGTTTCAACTCACCATCAGCAACAGCTGCTGCTTTTCAATTAATCATCAAAATC 930
Db 184 ATGGATCATTTGTTTACGACTCTCTTCCAACTGCTGTTGCAATTAATCCAAATACAACG 243
QY 931 CTGGTTGCTTAATTAATTTAAATTTCACTTTTGGCAAAAGTTTGGTAAATGAGTCCCAACAG 990
Db 244 ACCAAGCCCTTCAATACCTAAATTTGCTTTGTGAGTAAATTTGGCAGTGCAGTACCAGCA 303
QY 991 TTTATCCTCATGATTTATTTATTCGACTTTTTCGACTTTTATGTTGACACAATTTGAAAGATTA 1050
Db 304 TGTATCTTCAATTTGATGATTTGTCAGCTTTTCAATGGTGGACGCGCTTGAAGAAATGGGA 363
QY 1051 TTTTCACCACTTTCAGAGTGGAAATTAAGAAATTTTACATGAACACATACAGATGTTGGG 1110
Db 364 TTTCTCAGCGCTTTGTTCAGTGAATAGAAAGCATCTCGACATGGCATTAATTTGCTGTT 423
QY 1111 TGGAACGATCAGACAAATATTTTCATGGATGTTTGTAAATGCTGTTTGTAGCCTTTTCGCTTAT 1170
Db 424 TACAGAAAGATGAGGAATCATGATGGACATAGCAACATGTCATATGGCATTTTCGCTTT 483
QY 1171 TAAGGATCAATGGGTATGAAAGTTTCCAGATTCATTTGCTGAAATTAATTAAGATTAAG 1230
Db 484 TGAGGATGAATGGTTACAAATGTTTCTCAGATGAGCTGTCTCAGCTGCTGGAGCTTCCA 543
QY 1231 CTTTGAAGACGAATATGACAGCTCTTGAAG----- 1260
Db 544 CTTTCCATGATTCATACAAAGGATATTTAAATGATACAAATCCCTACATGGAATTTGTACA 603
QY 1261 -----CATATCATGGGTCAACATATATATATACCA 1288
Db 604 AGACCTCAAAAGTCACCTTATCAGAAAACGATCTGATCTTAGATCGCATAGGTTCTCTGTT 663
QY 1289 AGAGGATTTATCTTCTGGAAAAACAAATCTTGAAGTCAGCTGATTTCTCTCAAGAGATTAAT 1348
Db 664 CTGGCAACTTATTTGAAGGATAAGATGCTGTAGTAGGGTGCAGAAAAGACTTCGATTTTG 723
QY 1349 ATCCACTGATTCAAACAGCGCTTTCTTAAATTAATTCACA----- 1386
Db 724 GAGAGGTGCTGCAAAAAAAATTTAAATTTCTCAATTTTTCACCTGGAGGTTCAAGTTATGTC 783
QY 1387 -----AAGAGGTGGAAAAATGCTCTTAAGTTCCCTTATCAATACCGGTTTAGAA 1433
Db 784 TGTGTTTTGTGATTTTCAGATGGAGTATGCTGTTAAATTTTCCCTTGTATTTCCACACTGGAG 843
QY 1434 CGCATAAACACTAGACGAAATATACAGCTTTTACATGTTAGAGCAATACAGAAATCTTGAAA 1493
Db 844 CGTCTAGAACACAAAGAGAAACATTCGAACATTTTGTATGCTTGGGGTTTCTCTGATGCT---A 900
QY 1494 ACTACATATCACTCATCAATATTAAGTAACTGATTAACCTGATTAAGTTGCTGTTGAAGAT 1553
Db 901 ACAACAAAATCTCTCATTTTTCGATCAATCAAGAAATCTTACGCTTTGGCAGTCGAGAT 960
QY 1554 TTTCTACACCTGCGCAATCTATTTTATCGTGAAGAAATTAAGAAAGGCTTTGAAAGGTGGGTA 1613
Db 961 TTCAGTTTTCTCTCAAGCGTTTACCGGATGAATTCGCGCATCTTCATAGTTGGGTGAAG 1020
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1614 GAGAAATAGTTGGACCAAGCTCAAGTTTGTCTAGGCAAAAGACCGCTACTGTATTTCTCT 1673
1021 GAGAACAGCTGGACCAAGCTACAAATTTGTCTCGGCAAGAACTGACATATTTCTATCTGTCT 1080
1674 GTTGTGCAACACATTTTGTCTCCGAATATACAGATGCGGTATTTATCATGGGCAAAAT 1733
1081 GCTGTGCTACCGTATTTTCTCTGAATTTGTCTGACGCTCGCATTTTCATGGGCAAAAT 1140
1734 GGCATATTAACACTACAGTAGTTGATGACTTTTGTATATCGTGTGATCAATCGATGATG 1793
1141 GGTGCTCTCAACTGTGGTGTGATGACTTTCTTGATGTTGGTGTGATCAAAAGAAATTA 1200
1794 ACCAACTGATTCATGTTGAAATGCAATGTAGATGTCACAAGGATGTTGTTCA 1853
1201 GAAACCTGTAGCACTAGTTGAGAAATGCGATGCGCACCACGATGATGTTCTATTG 1260
1854 GAGATGTTCCGATTTTATTTTGTAGCAATTAAGATGCAATCTGTTGGATGAGATGAA 1913
1261 GAACAGGTGAAATAGTATTTTCTGCTATTTATACCAACAGTGAACCATCTTGGAGCAATG 1320
1914 GCTTTTAAATGGCAAGCGCGGATGTAACCTAGCATGTTATTCAAACTGTTGGTGGAACTA 1973
1321 GCTTCTGCAACAAGCGCGTGTCTTACAAACCACTAGTAGAAATATGGCTGGATTTG 1380
1974 ATCAATAGTATGTTGAGAGAGCTATATGCAAGAGATGCTTTATGTGCCAACATTAAT 2033
1381 TTAAGATCTATGATGTCGAGGAGATGCGAGATGCGCAATATATGACCAACATTTGAA 1440
2034 GAATATATGGAACCGTCTACGTGTCAATTTGCAATTTAGCCCGATTTGCAAGCGCGTATT 2093
1441 GAATACATGACAAATGCTGTGCTCATTTTGCACTGGGCGCAATTTGTGCTCCAGCATTTG 1500
2094 TACTTTGTGGGCGCAATTTATCAGAGGAGATTTGTTGAAGCTCTGAAATATCAATCTTA 2153
1501 TATTTTGTAGGCAAGAGCTATTTAGAGCATGCTGTCAAAGATGAAGAGTACGATAAATTA 1560
2154 TTTAAGCTATAGACGCGAGGCTCGACTTCTAAACGATATCCATAGCTTCAAGAGGAA 2213
1561 TTTAGGCTAGTAGACCTTCGGGAGGCTCTCAATGACTACCAAGTTTAGAGAGGAA 1620
2214 TTTAAGAGGCAAAATTAACCGCGTAGCAATTTGATTAACCGAGAAAGTGGGAA 2273
1621 GGCAACCGAGGAGCTGATAGTTGTTCTCTACTTTGTGCTCCACAGTGGTGTCTATG 1680
2274 GTGGAAGAGAGTTGTGGAGGAGATGATGATGATGATTTAAACCAAGAGGAAAGATTA 2333
1681 TCCATAGAGCCGCTAAAGAGGCAATGCAAGTCCATAGACGTTGTAGGAGAGACTTG 1740
2334 ATCAAAATTAATTTTGAAGAAATGTTAGCATTTGTTCTTAGAGCTTTGAAGATGCAATTT 2393
1741 CTAAAGTTGGTTCT---CAGGAAGAAAGTGTGTTCTTAGGCCATGCAAGGAGCTCTTC 1797
2394 TGGAAATGTTGTACGCTGTTGAAATTTTATGCAAAACGATGACGGGTTTA 2445
1798 TGGAGATGTTGAATACCTTACCTGTTTACTCTCAGAAATGATGATTA 1849

RESULT 14
US-10-259-194A-107
; Sequence 107, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Ghaseemian, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas

APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70029-NP
CURRENT APPLICATION NUMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/370,620
NUMBER OF SEQ ID NOS: 662
SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
SEQ ID NO 107
LENGTH: 2223
TYPE: DNA
ORGANISM: Oryza sativa
US-10-259-194A-107
Query Match 13.6%; Score 379.4; DB 6; Length 2223;
Best Local Similarity 54.5%; Pred.No.2.7e-78;
Matches 900; Conservative 0; Mismatches 676; Indels 75; Gaps 4;
QY 795 GGATACCTTGGCGTATATCTCTGAAGGACTCGGTAAATTTATATATGATTTGGATATGTTGAAG 854
DB 574 GAATATACGGCTTATGCTCTCAGAAGGATTAGGCAATATTTAGAACTGGAATGAATGATG 633
QY 855 AAATATCAGATGAAATATGTTCTGTTTCACTCACTCACTCACTCACTCACTCACTCACTCACT 914
DB 634 AAATTCAAAGAAAGATGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 693
QY 915 ATTAATCATCAATCTCTGTTGTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 974
DB 694 GTCCCAACTATGATGCCAAGCTCTCCAGTACTTAGACATGCTTCTGGCAAAATTTTGA 753
QY 975 AATGCACTCCCAACAGCTTTATCTCATGATTTATTTATCTCGACTTTCTATGTTGTGACACA 1034
DB 754 AGTGCACTGCCAGCGCTATCTCGCAATATTTTCACTCTCAGCTCTACATGTTGGATGTG 813
QY 1035 ATTGAAGATTTAGAAATTTTCAACCACTTTTCACTGAGTGGAAATTTAAATTTTAAATTTTAA 1094
DB 814 CTTGAAAGATGGAATATCTAGGCATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 873
QY 1095 ACATACAGATGTTGGTGGAAACGAGATGAGCAATATTTCAATGATGTTGTTGTTGTTGTTGTT 1154
DB 874 ACCTACAGTTGCTGGAAACGAGGATGAGAAATTTGCTTGCATGCAATGCAATGTTGGG 933
QY 1155 TTAGCCTTTTGGTTTAAAGGATCAATGGGTATGAAATTTTCCCGAGATCCATTTGGCTGAA 1214
DB 934 ATGGCATTTTGGTATGTTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 993
QY 1215 ATTACTTAATGAAATAGCTTTTGAAGAGCAATATGCACTGCTTTTGAATATATATATATATAT 1274
DB 994 TTTTCT-----GAACTTTCAAGTTTCCCAATTTCA 1023
QY 1275 CATATATTATACCAAGAGGATTTATCTCTGTTGAAACCAATCTTGAAGTCACTGATTTTC 1334
DB 1024 CTTCAAGGATATCTGAATGATCAAGATCTTTTATTAGATTAATATAGGCTTTCAAAAGTC 1083
QY 1335 CTCAAGAGATTAATATCCACTGATTTCAACAGGCTTTTCTAAATTTAAATTTTCAAAAGAGGTG 1394
DB 1084 -----AGTATCGCAAGAAAGGAGTTT 1104
QY 1395 GAAATGCTTTAAGTTCCCTATCAATAACGTTTGAAGCAATCACTAGACGAAAT 1454
DB 1105 GAATATGCTTTGAAATTTCCCTTCTATACCATCTTGGATCGTCTAGACCAATAAAGAAAT 1164
QY 1455 ATACAGCTTTTACATGTTAGCAATACAGAAATTTCTGAAACTACATATCTCATCAAT 1514
DB 1165 ATCGAAATTTTGAATATTAAGCAATTAAGCAATGCTAGAAACAGCT---ACTTGCCATGT 1221
QY 1515 ATTAGTAAACACTGATTTACCTTAAGGTTGGCTGTTGAAAGATTTTCTACACCTGCGCAATCTATT 1574

Db 1222 CATTCCAAATGAAGAAATCAATGGCTTGGGTGTGAGAGATTTTAGTAGCTCTCAGTTTAT 1281
Qy 1575 TATCGTGAAGAAATTAAGAGGTCTTGAAGAGTGGGTGTGAGAGAAATGAAGTTGACAGCTC 1634
Db 1282 TTCCRAAGAGAGCTGCAGCAACTCAACAGCTGGGTGAAGAGAGCAGGTTGGATCAGCTG 1341
Qy 1635 AAGTTTGTAGGAAAAGACCGCTACTGTATTTCTCTGTGTCTGTCTGCAACACTTTTGTCT 1694
Db 1342 CAAATTCGACCGGAGAGTTGGAAGTCTATTTCTCTGTCTGTCTGCTACTCAATTTTCACT 1401
Qy 1695 CCGCAATATCAGATCGCGGTATTTTCATCGGCCCAAAATGAGCATATTAACACAGTAGTT 1754
Db 1402 CTGAACTGTCAAGTTCGCAATTTTGTGGGCCAAAATGAGCGTGTGCAACGGTCGTC 1461
Qy 1755 GATGACTTTTTGATATCGGTGTGATCAATCGATGAATGACCAACCTGATCAATGTGTT 1814
Db 1462 GACGACTTCTCGACGTTGGAGGATCAAAAGAGAACTCGAAAACCTCGTCGCAATTAGTT 1521
Qy 1815 GAAAAATGAATGTAGATGTGCAAGAGATTTGTTGTTCAGAGCATGTTCCGATTTTATTT 1874
Db 1522 GAGAAGTGGGCAAGAATGACAAAACCTGAGTACTACTCTGAAACAGTAGAGATTTGTGTC 1581
Qy 1875 TTAGCAATTAAGATGCAATCTGTTGGATTGGAGATGAAGCTTTTAAATGGCAAGCGC 1934
Db 1582 TCTGCAATTTTACTTCAACTAACAGCTTGGATCAATGGCTCTGTGATGACAGGCCGT 1641
Qy 1935 GATGTAACCTAGCCATGTTTCAAACTTGGTGGAACTAATGAATAGTATGTTGAGAGAA 1994
Db 1642 GATGTACCAACACCTTGTAGAAATATGCAAGAAATGCTGAGGTCATGATGACAGAG 1701
Qy 1995 GCTATATGCAAGAGATGCTTATGTCGCAACATTAATGAATGAATATGAAAGCGCTTAC 2054
Db 1702 GTAGAGTGGAGGAGAGCGCGTATGTGCCAACAGCAGAGAGAAATACATGGAATAATG 1761
Qy 2055 GTGTCAATTTGCATTAGCCCGATGTGCAAGCGGCTATTTACTTTGTGGGGCCCAATTA 2114
Db 1762 GTGACATTTGCACTGGGACCGGTGTGTCGCCAGCATTTGATCTGTTGGACCAAGATC 1821
Qy 2115 TCAGAGGAGATGTTTGAAGAGCTGTAATATCATATCATATTTAAGCTAATAGCAGCGAG 2174
Db 1822 CTTGATTTCTCATAGAGACCAAGATGCAGGAGTTGTTCCGGCTATAGCAATCT 1881
Qy 2175 GGTGCACTTCAACCATATCATAGCTTCAGAGGGAATTTAAGGAAGCGCAATTAAC 2234
Db 1882 GGCCTGCTCTGAAATGATGTCGAATCTTACGAGAGAGGCGAGCGCAAGCTGAAC 1941
Qy 2235 GCGGTAGCATTCGATTTGATTAACGAGAAAGTGGGAAAGTGAAGAGAGGTTGTGGAG 2294
Db 1942 AGCGTCTCTGCTTCCCTCCACAGTGGAGGCTCTGTCTCCATGGAAGAGGCTGTGAAG 2001
Qy 2295 GAGATGATGATGATTAATAAACAAGAGGAAGAAATTAATGAATTTTGAAGAA 2354
Db 2002 CAGATTCAGAGACCCATCGAGAAATCGAGGAGAGTTGCTGAA ---GCTGGTCTGTCAGC 2058
Qy 2355 AATGTAGCATTTGTTCTAGAGCTTGAAGATGCAATTTTGGAAACATGTGTCAAGGTTG 2414
Db 2059 AGAGGAGGCGCGTTCGAAGGCCATGACAGGAGCTGTTCTGAGCATGTGCAAGGTCGTC 2118
Qy 2415 AATTTTTTTTACGCAACAGTACGCGGTTTA 2445
Db 2119 CACTTCTTCTACTCGCGCGGAGCGGGTTCA 2149

RESULT 15

US-10-425-115-77869
; Sequence 77869, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 77869
; LENGTH: 2178
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_17103C.1
US-10-425-115-77869

Query Match 12.8%; Score 357.4; DB 8; Length 2178;

Best Local Similarity 54.8%; Pred. No. 4,1e-73;

Matches 793; Conservative 0; Mismatches 621; Indels 33; Gaps 3;

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Db 464 GTCCGATGTGCTTGAACAACATGGGATTTCTCGCATTTTGGTGGTGAATCAAGTGATC 523
Qy 1086 TTAGATGAACAACATACAGATGTTGGGTGGAAACGAGATGAGCAAAATATTCATGGATGTTGA 1145
Db 524 CTGTGACAGACATACAGATGTTGGTTACAGACACGAGGAAATATGACGACACAACG 583
Qy 1146 ACATGTGCTTTAGCTTTTCGGTTATTAAGGATCAATGGGTATGAAGTTTCCCGAGATCCA 1205
Db 584 ACATGTGCGATGGCATTTGCTATTTAAGGATGAATGGAATCAATGCTCTCTCTGATGAG 643
Qy 1206 TTGGCTGAAATTTACTAA-----TGAAATTAGCTTTTGAAGAC 1241
Db 644 TTGTATCATGTTTGTGAAGCTTCGAGATCCCAATAATTCATTTGGAGGATATCTCAATGAC 703
Qy 1242 GAATATGACAGCTCTTGAACAACATATCATGCGT---CACATATATATPACCAAGAGGATTTA 1298
Db 704 ACAGAACCTTCTGTAGAAATTAACAAGGCTCTACAGTTAGTATCTCTGAAGACGAGTCT 763
Qy 1299 TCTTCTGGAACAAATCTTGAAGTCAGCTGATTTCTCAAAAGAGATAATATCCACTGAT 1358
Db 764 ATCTCTGGATAGCATAGGCTCAAGGTCAAGTACTTACTGAGGGAACAACCTAGAGTCTGCT 823
Qy 1359 TCAACACAGCTTTCTAATTAATTCACAAGAGGTGGAAATGCTCTTAAGTTCCCTATC 1418
Db 824 GGTGCTCTACGAAATCTCTTCACTCTTTAAAGAGGTGGAAACATGCTCTGACGCTCCCTTC 883
Qy 1419 AATACCGGTTTAGAACGCAATAACACTAGACGAAATATATACAGCTTTTACATGTAGACAAT 1478
Db 884 TACACCAACATTTGACCGCTACACCATAGGTGGAAACATCGAAATTTCAATATATAGAG 943
Qy 1479 ACAAGAAATTCGAAACACTACATATCACTCATCAAAATATTTAGTAACACTGTACCTAAGG 1538
Db 944 CAGCACATGCTAGAGACACCATACTTGTCAAATCAACATACCAGTAGAGATATCTTAGCG 1003
Qy 1539 TTGGCTGTTGAAGATTTCTACACCTGCCAATCTATTTTACGTGAAGAAATTAAGAGTCTT 1598
Db 1004 TTGAGTATTTAGAGACTTTCAGTTTCTCTCAGTTTACTTACAGCAAGAACTTCAACATCT 1063
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Qy 1659 TACTGTATTTCTCTGTGCTGCAACACTTTTCGTCTCCGAAATATATCAGATGGCGTATTT 1718
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Db 1304 GTTCAGTCTCTACTCAGACAGTAGAGATATATTTTCTTCAATTTATGACTAGTTAAC 1363
Qy 1899 TGGATTGGAGATGAAGCTTTTAAATGGCAAGCGCGGATGTAACCATGTTTATTCAA 1958
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Db 1364 CAACCTTGGTGAAGAGGCTTCTTTGGTACAAGACCGCAGTATTACAAACACCTAGTAGAA 1423
Qy 1959 ACTTGGTGGAACTAACTAGTATGTTGAGAGAGCTATATGCAAGAGATGCTTAT 2018
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Db 1424 ATATGGTGGATTTGCTAAAGTCTATGATGACAGAGTAGAGTGGCGTTTGAGCAATAT 1483
Qy 2019 GTGCCAATTAATGAATATATGAAACCGCTTACGTGTCATTTGCAATAGGCCCGATT 2078
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Db 1484 GTGCCACAGAGAGGATACATGATAAATGCACTTTTAACATTTGGACTAGGCCCATTT 1543
Qy 2079 GTCAAGCGGCTATTTACTTTTGGGGCCCAAAATTAACAGAGAGATGTTTGAAGCTCT 2138
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Db 1544 GTATTGCCAGCATATATTTTGGTGGCCAAAGATCTCAGAGTCTATTGTTAAAGATCCA 1603
Qy 2139 GAATATCATATCTATTTAAGCTAATGAGCAGCGGTCGACTTCTAAACGATATCCAT 2198
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Db 1604 GAATATGATGAATTTGTTCAAACTGATGAGCACATGTGGTCGCCCTTTGAATGATGTTCAG 1663
Qy 2199 AGCTTCAAGAGGGAATTTAAGGAAGGCAATTTAAACCGGTAGCATTTGCAATTTGAGTAAC 2258
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Db 1664 ACTTTGAGAGGGAGTACACGAGGGCAGTTGAATAGTGTCTCTCCTCGTTCTTCAT 1723
Qy 2259 GGAGAAAGTGGAAAGTGGAAAGAGAGGTTTGGAGGAGATGATGATGATTAATAAAC 2318
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Db 1724 GGTGGCTCCATGTCCATATCAGACGCCCAAGGAATTTACAGAGCCCATAGACACATGC 1783
Qy 2319 AAGAGGAAGAAATTAATGAATTAATTTTGAAGAAATGCTAGCATTTCTCTAGAGCT 2378
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Db 1784 AGAAGACACCTCCTTAAGTTTCTTCGTGAAGAAAGTG-----TTGTTCTTAGGCC 1837
Qy 2379 TGTAAGATGCATTTTGAACATGTGTCAGTGTGAAATTTTACGCAAAACGATGAC 2438
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Db 1838 TGCAGGAATTAATTTTGGAAATGTCAGGTGTGCTACTTCTTCTACTCGACGCGGAT 1897
Qy 2439 GGGTTTA 2445
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Db 1898 GGGTTTA 1904

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OM nucleic - nucleic search, using sw model

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Title: US-10-041-018-361

Perfect score: 2792

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Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfileseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	782.2	28.0	2658	3	US-08-727-308-2
2	782.2	28.0	2658	3	US-08-727-308-3
3	453.2	16.2	2403	3	US-09-614-912-23
4	238.2	8.5	1157	3	US-09-614-912-33
5	194.8	7.0	2861	3	US-09-398-395A-55
6	194.8	7.0	2861	3	US-09-887-586A-55
7	194.8	7.0	2861	3	US-09-895-752-55
8	194.8	7.0	2861	3	US-09-903-012B-55
9	194.8	7.0	2861	3	US-09-900-797-55
10	194.8	7.0	2861	3	US-09-893-820-55
11	194.8	7.0	2861	3	US-10-041-007-3
12	153.8	5.5	2700	3	US-09-315-861-1
13	153.8	5.5	2700	3	US-09-398-395A-43
14	153.8	5.5	2700	3	US-09-887-586A-43
15	153.8	5.5	2700	3	US-09-895-752-43
16	153.8	5.5	2700	3	US-09-903-012B-43
17	153.8	5.5	2700	3	US-09-593-253-1
18	153.8	5.5	2700	3	US-09-797-43
19	153.8	5.5	2700	3	US-09-893-820-43
20	139.2	5.0	531	3	US-09-614-912-27
21	133.8	4.8	2241	3	US-10-041-007-36
22	133.8	4.8	2388	3	US-10-041-007-36
23	133.8	4.8	2445	3	US-10-041-007-34
24	133.8	4.8	2622	3	US-10-041-007-32

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Sequence 25, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 1, Appli
Sequence 15, Appl
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Sequence 45, Appl
Sequence 45, Appl
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Sequence 45, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 14, Appl
Sequence 39, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 13, Appl
Sequence 12, Appl
Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-727-308-2
; Sequence 2, Application US/08727308
; Patent No. 6020176
; GENERAL INFORMATION:
; APPLICANT: YUJI KAMIYA et al.
; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,308
FILING DATE: October 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2658 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-727-308-2

Query Match 28.0%; Score 782.2; DB 3; Length 2658;
Best Local Similarity 61.3%; Pred. No. 2.3e-191;
Matches 1390; Conservative 0; Mismatches 823; Indels 54; Gaps 6;

Db 2381 GAAATTGATGCCATTGTGAATCTATTTTACATGGAAGATGATGGGTACACTTCAAAATAG 2440
Qy 2456 GATCTTGATACGTGAGACATCATTTCAACCCGTTGGTGGCTTG 2502
Db 2441 GTTGATGAACACTGTAAAGCCATGTTTGAACAACCCATGGATCTGG 2487

RESULT 2
US-08-727-308-3
; Sequence 3, Application US/08727308
; Patent No. 6020176
; GENERAL INFORMATION:
; APPLICANT: YUJI KAMIYA et al.
; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,308
; FILING DATE: October 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2658 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-727-308-3

Query Match 28.0%; Score 782.2; DB 3; Length 2658;
Best Local Similarity 61.3%; Pred. No. 2.3e-191;
Matches 1390; Conservative 0; Mismatches 823; Indels 54; Gaps 6;

Qy 275 AACTAATCCCACTAAATCTGATCACTGATACACCAAGAAGCGATCCAAAAACAGTTTAA 334
Db 236 AACTAAAACCTGGAGCTTTGCACCTTTGAAGAAACAAAAGAAAGAAATTAAGAAATTTGTTTGA 295
Qy 335 AAATGTAGAAATTTCTGTTTCTTATATGACAGCATGGGTAGCCATGGTCCCTTCTCC 394
Db 296 CAAGTTGAACTTTGAGTTTCTGATATGATCTGCAATGGGTGGCAATGGTTCTTCTCC 355
Qy 395 AAATCAACCAAAATCGCTTTGTTTCCCTGAGTGTCTCAATGGTTTAAATTAATCAAGCT 454
Db 356 AACTCTCTCAACCAACCTCTTTTCCCGAGTGTATAAATCTGGGTATTAGATAGTCAACA 415
Qy 455 TAATGATGGTTCAATGGGGTCTTGTATATCACTCATATATCAATATCAACCCGTTGCTTAA 514
Db 416 TGCTGATGGTCTATGGGGCTTACTCCACAAC-----GATCAGTTGCTGATGAA 463
Qy 515 AGATTCTCTATCTCAACATTAGCATGTTGTCATTAAAGATGGAATGTTGGGA 574

Db 464 GGCCAAATCTCTTATCTACATTAGCATGTGTTCTTACTCTTAAGCGGTGGAATATTGGCA 523
Qy 575 AGATCAAAATAAAGGTCTTAAGTTTATTAGTCAAAATCTTGTCTCAGCTACTGAAAA 634
Db 524 TGATCATATGAGCAAGGCCCTTGATTTTATCAAGTCTAAATATAGCTTTCAGCTACTGATGA 583
Qy 635 AAGTCAACCATCTCCCAATTGGTTTGGACATCATATTTCCTGGTGGTTGCTGAGTATCGAA 694
Db 584 GAACCAAGCTTCTCCGGTGGGATTTGACATATTTCCTCCCTGGCATGATTTGATGATGCTAA 643
Qy 695 AAATTTGGACATAAAACCTCTTTCAAAACAAACAGATTTTATGTTTGTGCTTACATAAGAG 754
Db 644 AGACTTGAATTTGAATCTACCTTGGCACGACGACGCTGGATGCTTGGTCTCGAAAGAA 703
Qy 755 GGAATTTGGAGCAAAAA-----AGATGCCATTCAAAATGAGATGGATGGATGCTTGGCGTA 808
Db 704 AGATTTGGAGCTGAGAAAGCTGCAGAAAGCAACTCGAAGTGGGAAAGCCCTATTATTAGCGTA 763
Qy 809 TATCTCTGAAGGACTCGGTAATTTATATGATTCGGAATATGCTGAAGAAATATCAGATGAA 868
Db 764 TGTTTCAAGGAATTTGGAAGTTACAGACTGGGATATGGTCATGCAATATCAAGAGAA 823
Qy 869 AAATGGTCTGTTTCAACTCAGCATCAGCAACAGCTGCTGCTTTTCAATTAATCATCAAAA 928
Db 824 GAATGGATCACTGTTTAAATTTCTCCATCCACTACGGCAGCGGCTTTTATGATAGATAAAATGA 883
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Db 884 TGATGGCTGTTTGAATTTATCTCGCTCACTTTACAAAAGTTTGAATGGCTCAGTTCCCAAC 943
Qy 989 AGTTTATCTCATGATTTATTTATCCGACTTTCTATGTTTGAACAAATTCAGAAATGATAGG 1048
Db 944 AATATATCTCTTGATATATATCTCGATTACACATGGTTGATAGCCCTTCAAAAATTCGG 1003
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Qy 1109 GGTGGAACGAGATGAGCAATAATTTATGATGTTTGTAAATGATGCTTTTACGCTTTCGGTT 1168
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Qy 1169 ATTAAGGATCAATGGGTATGAAAGTTTCCCGAGATCCATTCGCTGAAATTAATAA----- 1222
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Db 1244 GGCCTCTCAGATTTATCAGCACCCCGATGAATGTTCTGCGAAAAATATAAACTCTTGAC 1303
Qy 1325 AGCTGATTTCTTCAAGAGATATATCCACTGATTCAAACAGAGCTTCTAAA----- 1376
Db 1304 TAGTCGTTTCTCGAAGCATGGATTATCTAGTGATTCAGTTTGGTCTGATAGAACCGATAG 1363
Qy 1377 -TTAAATTCAAAAAGAGTGGAAAAATGCTCTTAAGTTTCCCTTATCAATACCGGTTTGAACG 1435
Db 1364 TGTGTTTAAACAGAGGCTGTTAATGCTCTTGAAGTTCCCTTAATAATGCAACTCTAGAAGC 1423
Qy 1436 CATAAACACTAGACGAAATATACAGCTTTTCAATGTAGACAAATACAAAGAAATTCGAAAAAC 1495
Db 1424 CCTAATAAGTAAGAGGGCAATGGAAGTTACAGTGGAGACATTTGTAGAGGATTTCAAAATC 1483
Qy 1496 TACATATCACTCATCAATATTTAGTAACACTGATTAACCTTAAGGTTGCTGCTGTAAGATTT 1555
Db 1484 GCATATGCTGCTTAAATTTTGGCCATCAAGATTTTCTGGAACCTTCTCTAGAGGATTT 1543
Qy 1556 CTACACTGCGCAATCTATTATTATCGTGAAGAAATTAAGAGGTCTTGAAGGTGGGTGGTGA 1615

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1604	DB	AAACAAATTGGACGAGTTGAAATTTTTTCAGACTGCACTTAGGGTACTGCTATTTTGTCTGC	1663
1676	QY	TGCTGCAACACTTTCGTCTCCGAATTTACAGATGCGCGTATTTTCATGGGCGCAAAATGG	1735
1664	DB	GGCAGCGACCCCTTACTGATCTCGAACTTCATGATGCTCGCATAGCATGGGCACAAAATGG	1723
1736	QY	CATATTAACTACAGTAGTGTGATGACTTTTTTTTGATATCGGTGGTACAATCGATGAATTTGAC	1795
1724	DB	TGTGCTCAGACCGGTGTTGATGTTCTATGATGGTGGAGATCTGAAGAGGAATTTGGA	1783
1796	QY	CAACCTGATTTCAATGTGTTGAAAAATGGAATGTAGATGTGCACAAGAGTATGTTGTTCCAGA	1855
1784	DB	TAACCTTATAGAAATTGTTGGAAAGTGGGATCTGTATGGGGAAGTGGTTACTGTTCCAA	1843
1856	QY	GCATGTTCCGATTTATTTTTAGCATTTAAAGATGCAATCTGTGTTGGAATTTGGAGATGAAGC	1915
1844	DB	GGACGTTGAGATTGTTCTTGCACTGCACAGCACAGATTGTTGTAATAGAAATAGAAAGAGC	1903
1916	QY	TTTTTAATTCGCAAGCGCGCATGTACTAGCCATGTTATTTCAAACCTTGGTTGGNACTAAT	1975
1904	DB	TTTAGTATGGCAAGGACGAGTGTATTAGGAATGTTTATCGATGGTTGGTTGGCTCTGCT	1963
1976	QY	GAATAGTATGTTGAGAGAAGCTATATGCAAAAGAGATGCTTATGTGCAACATTTAAATGA	2035
1964	DB	GAAGTGATGAGAAAGAAAGCTGNAUGGTGCACAAATAGGTAGTGCCATCAATGGGTGA	2023
2036	QY	ATATATGGAAAAACGTTTACGTGTCATTTGCAATTAGGCCGATTTGTCAAGCCGCTATTTA	2095
2024	DB	ATATATGCAACAAGCCCATGTATCAITTCGGTTGGGACCTATAATCTTCCAATGCTCTT	2083
2096	QY	CTTTGTGGGGCCCAAAATTTACAGAGGAGATTTGTGAAGCTCTGGAATATCATATCTATT	2155
2084	DB	CTTTGTTGSAACCTAAACTCTCAGAGGAAATGATTTGGAAGCTGTGAATACAGAAAGTTATA	2143
2156	QY	TAAGCTAATGAGACGACGAGGTGCAGCTCTTAAACGATATCCATAGCTTCAAGAGGGAATT	2215
2144	DB	TAAGCTGATGAGCACTGCTGGTTCGCTTTAAGATGATATTCGATCTTTACGTAGAGATG	2203
2216	QY	TAAAGGAAGCAAAATTAACCGCGTACGATTGCAATTTGAGTAACGGAAGAAAGTGGGAAAGT	2275
2204	DB	CAAAGAGGAAAGCTGAATTTCTGCTCTGTGATGATTTGATGGCGGTGGTAATGTCCAC	2263
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2264	DB	CAAAGAGGAGGCCATTGAACCAATTAAGGGGATTTTGGAGGGCGCATAGAGAGCTGCT	2323
2336	QY	GAAATTAATTTTTGAACAAAATGTTAGCATTTGTTCTCCTAGAGCTTGTAAAGATGCATTTTG	2395
2324	DB	GGGGTTAGTTTTCGAGGAGAACCTACA---TTCCAAGAGCTGTGAAGATTTGTTCTG	2380
2396	QY	GAACTATGTCACGTGTTGAATTTTTTTTACGCAACGATGACGGGTTTACTCGAAACAC	2455
2381	DB	GAAATTGATGCCATTGCGAATCTATTTTACATCGAAGATGATGGGTACACTTCCAATAG	2440
2456	QY	GATCTTTGATACGTGTGAAGGACATCATTTTCAACCCGTTGGTGGTTG	2502
2441	DB	GTTGATCAACACTGTATAAGCCATGTTTGAACCAACCACTGCATCG	2487

RESULT 3

US-09-614-912-23

; Sequence 23, Application US/09614912

; Patent No. 6677502

GENERAL INFORMATION:

APPLICANT: Allen, Steve

; APPLICANT: Rafalski, Antoni

APPLICANT: Orozco, Buddy

APPLICANT: Miao, Gou-Hau

APPLICANT: Famodu, Omolayo O.

```

; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 23
; LENGTH: 2403
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1049)
; US-09-614-912-23

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Db 612 ATGGGAATTTCTCAGCGCTTGTGTCAGTGAATGAAAGCATCCTGGACATGGCATACAAT 671
Qy 1104 TGTGGGTGGAACAGAGATGACCAATATTATGATGATGTTGTAACATGCTGTTAGCCCTTT 1163
Db 672 TGCTGGTTACAGAATGATGAGAACTCATGATGACATAGCAACATTTGCAATGGCAATTT 731
Qy 1164 CGGTTATTAAAGGATCAATGGGTATGAAAGTTTCCCCAGATCCATTGGCTGAAATTTACTAAT 1223
Db 732 CGCCTTTTGAGGATGATGGTTACGATGTTCTCTCAGATGAGCTGTCTCAGTTGCTGGA 791
Qy 1224 G-----AATTAGCTTTGAAAGCAAGATATGACGCTCTTTGAA 1259
Db 792 GCTTCCACTTTCCATGATTCACACAAGGATATTTAAATGATACAAATCCCTACTGGA 851
Qy 1260 ACATATCATGGTCACA---TATATTATACCAAGAGATTTATCTCTCGAAGAAACAATC 1316
Db 852 TTGTACAAGACCTCANAAGTCACCTTATTCAGAAACGATCTGATCTTTAGATGCGATAGGT 911
Qy 1317 TTGAAGTCAGCTGATTTCTCAAGAGATAATATCCAC----- 1354
Db 912 TCCTGGTCTGGCAACTTATTGAGGATAAGATGCTGTAGTAGGTGCAAAAGACTCGA 971
Qy 1355 -----TGATTCAAACAGGCTTTCTAAATTAATTCACA- 1386
Db 972 TTTTGGAGAGATGCTGCAACCAAAATTTAAATTTCTCATTTTCACTTTGGAGGTTCAAGTT 1031
Qy 1387 -----AAGAGGTGAAATGCTCTTAAGTTCCTTATCAATACCGGT 1427
Db 1032 TATGTCGTGTTTGTGNTTTCAGATCGAGTATGCTGTGTTAAATTTTCCCTGTATTCACA 1091
Qy 1428 TTGAACGCATAACACTAGACGAAATATACAGCTTTTACAAATGATAGCAATACAAAGATT 1487
Db 1092 CTGGAGGCTTAGACACAGAGAAACATCGAACATTTTGTATGCTGGGGTCTCTGATG 1151
Qy 1488 CTGAAACTACATATCACTCATCAAAATPATTAGTAACACTGATTAACCTAAGGTGGCTGTT 1547
Db 1152 CT---AACAAACAAATCCTCATCTTTTCGTATCAATCAAGAAATTCCTAGCTTTGGCAGTC 1208
Qy 1548 GAAGATTTCTACACCTGCCAATCTATTTATCGTGAAGAAATTAAGGTCTTGAAGGTGG 1607
Db 1209 GAAGATTTCTAGTTTCTCTCAACGTTTCTACCGGATGAACCTTCGGCATCTTGTAGTTGG 1268
Qy 1608 GTGTAGAGATAAGTTGGACCACTCAAGTTTCTAGGCAAAAGACCGCTACTGCTAT 1667
Db 1269 GTGAGAGAAACAGCTGGACCACTCAATTTGCTCGGCAAAACAGCAATATGCTAT 1328
Qy 1668 TTCTCTGTTGCTGCAACACTTTCTGCTCCGAATPATTACAGATGCGGTATTTTCATGGGCC 1727
Db 1329 CTGCTGCTGCTGCTACCGTATTTTCTCTGAATTTGCTGAGCGCTGCAATTTTCATGGGCC 1388
Qy 1728 AAAAAAGCATATTAACACTACAGTATGATGACTTTTGTATATCGTGGTACATCGAT 1787
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Qy 1788 GAATTGACCACTGATTTCAATGTTGAAATGGAATGTAGATGTCGACAGGATGTTGT 1847
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Qy 1848 TGTTCAGAGCATGTTCCGATTTTATTTTATAGCATTAAGATGCAATCTGTGTGATTTGGA 1907
Db 1509 TATTCGGAACAGGTGAAATAGTATTTTCTGCTATTTATACACAGTGAACCATCTTGA 1568
Qy 1908 GATGAGCTTTTAAATGCGAAGCGCGGATGTAAGTACGCAATGTTATCAACTGTTGGT 1967
Db 1569 GCAATGCTTTCTGAGCACAAGGCGGTGCTTACAAACCACTAGTAGAATAATGCTG 1628
Qy 1968 GAACATATGATGATGTTGAGAGAGCTATATGGAACAGAGATGCTTATGTGCCAACA 2027
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Db 1689 GTTGAAGATATACATGACAAATGCTGTTGTCTCAATTTGCACTGGGCCCAATTTGTCTCCCA 1748
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Qy 2148 AATCTATTAAAGCTTAATGAGCAGCGAGGTCGACTTCTTAAACGATATCCATAGCTTCAAG 2207
Db 1809 AATATTATTAGGCTTAGTGACACTTGGGGGAGGCTCTCAATGACTACCAAAAGTTTAGAG 1868
Qy 2208 AGGAATTTAAGAGGCAAAATTAACCGCGGTAGCATTTGATTTAGTAACGGAAGAAGT 2267
Db 1869 AGGAAGGCAACCAAGGGAAGCTCAATAGTGTCTCTACTTTGTGCTCCACAGTGGTGT 1928
Qy 2268 GGAAGAGTGAAGAGAGGTTGTGGAGGAGATGATGATGATGATTAAACCAAGAGGAA 2327
Db 1929 TCTATGTCATAGAGCCGCTTAAAGGCAATGAGAAAGTCCATAGAGCTGTCTAGGAGA 1988
Qy 2328 GAATTAATGAATTAATTTTGAAGAAATGCTAGCATTTGTTCTTAGAGCTTTGTAAGAT 2387
Db 1989 GACTTGTCTAAGTTGTTCT---CAGGAAGAAAGTCTGTCTCTAGGCCATGCAAGGAG 2045
Qy 2388 GCATTTTGAACATGTGTACGTTGCTGTTGAAATTTTTTTTACGAAACGATGACGGGTTTA 2445
Db 2046 CTCTTCTGGAAGATGTGTAAGATACTTCACCTGTTTACTCTCAGAAATGATGGATTTA 2103

RESULT 4

US-09-614-912-33
; Sequence 33, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafaleki, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (40)
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; NAME/KEY: unsure
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; LOCATION: (1105)..(1106)
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; NAME/KEY: unsure
; LOCATION: (1136)..(1137)
; NAME/KEY: unsure
; LOCATION: (1155)
US-09-614-912-33

Query Match      8.5%; Score 238.2; DB 3; Length 1157;
Best Local Similarity 58.1%; Pred. No. 3e-51;
Matches 433; Conservative 0; Mismatches 303; Indels 9; Gaps 1;

QY 505 CGTTGCTTAAAGATTCTCTATCTTCAACATTAGCATGTATTGTCATTAAAAAGATGGA 564
DB 54 CGGTCAACAANGATGTTCTCCTATCCACGTTGGCATGTGTTCTTGCGTTGAAGAGATGGA 113
QY 565 ATGTTGGGGAAGATCAAAATAAAAGGTCTAAGTTTATTGAGTCAAAATCTTGCTTCAG 624
DB 114 ATGTTGGCAGAGAGAAACAATTTGGAGAGGACTGCATTTTCATCGGAGGAATTTCTCTGTTG 173
QY 625 CTACTGAAAAAGTCAACCATCTCCATGTTGGTATTTGACATCATATTTCTGTTGCTTG 684
DB 174 CTATGACGAGCAGTTCACTTCTCTATAGGTTTCAACTTTCACCTTCTGTTGCTTA 233
QY 685 AGTATGCGAAAAAATTTGGACATAAAACCTCTCTTTCAAAACAAACAGATTTTAGTTGATGC 744
DB 234 GCCTCGGCATTGATATGGGTTTAGAATTTCTCTGTAAGACAAATGTATGTCGTGGCATTC 293
QY 745 TACATAAGAGGGAATTTGGAGCAAAAAG-----ATGCCATTCAAAATGAGATGGATG 795
DB 294 TTCACCGCGGAGATGGAATTTGAAAAGGCTGGCTGTGGATAGTTCTTTTGGAGAAAAG 353
QY 796 GATACTTGGCGTATATCTCTGAAGACTCGGTAAATTTATATGATGGAATATGGTGAAGA 855
DB 354 CATATATGGCTTTTATCCAGAAAGATTCGGAATATGCTGGAATCGGGATCAAGTTATGA 413
QY 856 AATATCAGATGAAAAATGTTCTGTTTCAACTCACCATCAGCAACAGCTGCTGCTTCA 915
DB 414 AGTTTCAGAGGAAGATGGATCATTTGTCAGCCTCTTCCACAACCTGCTGTGCAATTAA 473
QY 916 TTAATCATCAAAATCCTGGTTGTTCTTAATTTTAAATTCACCTTTTGGACAAGTTTGGTA 975
DB 474 TCCACAAATACACGACCAAGCCCTTCAATACCTTAATTTGCTTGTCAATGAATTTGGCA 533
QY 976 ATGCAGTCCCAACAGTTTATCCTCATGATTTTATTCGACTTTCTATGTTGACACAA 1035
DB 534 GTGCAGTACCAAGCAATGTATCCTTCAAGGGTACATTTGTGAGCTTTCAATGGTGAGCGCG 593
QY 1036 TTGAAAGATTAGGAAATTTTCCACACCAATTTCCAGAGTGGAAATTTAAATGTTTAGATGAA 1095
DB 594 TTGAAAAAATGGGAATTTCTCAGCGCTTTGTGAGTGAATATAAAACATCCTGGAATGG 653
QY 1096 CATACAGATGTTGGGTGGAACGAGATGAGCAAAATATTCATGAGATGTTGTAACATGCTT 1155
DB 654 CATACAAATTGCTGGTTTACAGAAAGATGAGGAATCATGATGGACATAGCAACATTTGCNA 713
QY 1156 TAGCCTTTCGGTTTATTAAGGATCAATGGGTATGAAGTTTCCCAGATCATTGGCTGAAA 1215
DB 714 TGGCATTCNCCTTTTGGANGATGANTGGTTACAATGTTTCTCCTCNGATGANTGCTGTACAG 773
QY 1216 TTACTAATGAATTAGCTTTGAAAAGA 1240
DB 774 TTGCTGGANTTCCACTTTCCATGA 798
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RESULT 5
US-09-398-395A-55
; Sequence 55, Application US/09398395A
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; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6468772, Joseph P.
; APPLICANT: Starke, Courtney R.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-398-395A-55

Query Match          7.0%; Score 194.8; DB 3; Length 2861;
Best Local Similarity 47.8%; Pred. No. 6.8e-40;
Matches 866; Conservative 0; Mismatches 857; Indels 87; Gaps 7;

QY 337 ATGAGAAATTTCTGTTCTTCATATGACACAGCATGGGTAGCCATGGTCCCTTCACAA 396
DB 337 ATGGCGAAACGAATCCCTCTGCGATATGACATGCTGGGTAGCAAGGATTTCCAGCAGTTG 456

QY 397 ACTCACCAAATGGCTTGTTCCTGAGTGTCTCAATGGTTAAATTAATAATCAGCTTA 456
DB 457 ATGGCTCTGACACCCCTCACTTTCCTGAGACGGTTGAATGGATCTTCAAAATCAGTTGA 516

QY 457 ATGATGTTTCATGGGTTCTGTTAAATCACATCAATCAATCAATCAATCAATCAATCAAT 516
DB 517 AAGATGGGTCTGGGGTGAAGGATTTCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 558

QY 517 ATTCTCTATCTTCAACATTAAGATGATTTGTCATTAATAAAGATGGAATGTTGGGGAAG 576
DB 559 ACAGAAATACCTGGTACATCTGCAATGATTAATTAATTAATTAATTAATTAATTAATTAAT 618

QY 577 ATCAAAATAAATAAGGTCTAAGTTTATTTAGTCAAAATCTTCTTCAAGTACTGAAATAAA 636
DB 619 CACAGTACAGAAAGGTATTAATTTCTTCAAGACACAGCTGGAAGATGGAAGATGAAG 678

QY 637 GTCACCATCT---CCCATGGTTTGGACATCATATTTCTCTGGTTTGGTTGAGTATGCGA 693
DB 679 CTGATAGTCTAGGCCAAGTGGATTTGAAATAGTATTTCTGCAATGCTTAAAGGAGCTA 738

QY 694 AAACTTGGACATAAACCCTCTTCAAAACAAACAGATTTTATTTGATGCTACATAAGA 753
DB 739 AAATCTTAGGCTTGGATCTGCTCTTACGATTTGGCATTTCTTGAACAAATCATCGAAAGC 798

QY 754 GCGAATTTGGAGCAAAAGATGCCATTAATGAGATGGAATG---GATACTTGG 804
DB 799 GGGAGGCTAGCTTTAAAGGATTTCCCACTGATGTTCTATGCGCTTCCAAACAGTTAT 858

QY 805 CGTATATCTCTGAAGGACTCGGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 864
DB 859 TGTATTTCTTGGAAAGGTTTACAGAAATAGTACTGCGCAGAAAAATAATGAATCTCAAT 918

QY 865 TGAATAATGTTCTGTTTCACTCACCATCAGCAACAGCTGCTGCTTCAATTAATCATC 924
DB 919 CCAAGGATGATCATTTCTCAGCTCTCCGCACTACAGCGGCTGATTTCTATGCGTACAG 978

QY 925 AAAATCTGTTGTTCTTAATTAATTAATTAATTTTGGACAAAGTTTGGTAAATGCGAGTCC 984

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DB 979 GGAACAAAAGTGCTTGGATTTCTTGAACITTTGTTGAAGAAATTCGGAACCAATGTCG 1038
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QY 1105 GTTGGGTGGAAACGAG-----ATGAGCAAAATATTATCATGATGTTTGAACAT 1149
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DB 1339 TTACAGACATGTTTAAAGCTCAATCGTTGTTTCAATGTTTCAATTTCCGGGAGAAACGATCA 1398
QY 1318 TGAAGTACGCTGATTTCT-----CTCAAAGAGATTAATAT 1350
DB 1399 TGAAGAGCAAAACTCTGTACCGAAAGGTATCTGAGGAATGCTCTGGAATAATGTGGATG 1458
QY 1351 CCACATGATTCACACAGCTTTCTAAATTAATTCACAAAGAGGTGGAATAATGCTCTTAAGT 1410
DB 1459 CTTTGAATAATGGGCTTTTAAAGAGATATTTGGGAGAGGTAGAGTATGCACTCAAT 1518
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QY 1471 TAGACATACAGAAATCTGAAACATACATATCACTCATCAATATTTAGTAACTACTGAT 1530
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QY 1591 AAGGCTCTGAAAGGTTGGGTAGAGAAATAAGTTTGAACCAAGCTCAAGTTTGTCTAGGCAAA 1650
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DB 1879 CCCATGATCTTTAGACGATCTTAAAGTTGTTTACAGAACTAGTCAAAAGATGGATCTAT 1938
QY 1831 ATGTGACAGAGATGTTGTTTACAGCATGTTCCGATTTTATTTTATTTTATGCAATTAAGATG 1890
DB 1939 CACTAG---TGGACCAAAATGCCAACAAATAATGAAATATGTTTGTGGGTTTCTTACAATA 1995
QY 1891 CAATCTGTTGGATTTGGAGATGAAGCTTTTAAATGGCAAGCGCGGATGTAAGTACTAGCCATG 1950
DB 1996 CTTTAAATGATATAGCAAAAGAGGACGCTGAGAGGCAAGGCGGATGTCGTAGGCTACA 2055
QY 1951 TTATTCAAACCTGGTTGGAACTAATGAATAGTATGTTGAGAGAGGCTATATGGAACAAGAG 2010

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Db 2056 TTCAAAAATGTTGGAAAGTCCAACTTGAAGCTTTACACGAAAGACGAAATGGTCTGAAG 2115

Qy 2011 ATGCTTATGTGCCAACATTAATAATGAATATATGAAAAACGCTTACGTGTCAITTTGCAATTAG 2070

Db 2116 CTAATAATGTGCCATCTTCAATGAATACATAGAGAATCGAGTGTGTCAATAGCAATTGG 2175

Qy 2071 GCCCGATTGT 2080

Db 2176 GAACAGTCGT 2185

RESULT 6

US-09-887-586A-55

; Sequence 55, Application US/09887586A

; Patent No. 6495354

; GENERAL INFORMATION:

; APPLICANT: Chappell, Joseph

; APPLICANT: No. 64953541, Joseph P.

; APPLICANT: Starks, Courtney M.

; APPLICANT: Manna, Kathleen R.

; TITLE OF INVENTION: SYNTHASES

; FILE REFERENCE: 07678-025001

; CURRENT APPLICATION NUMBER: US/09/887,586A

; CURRENT FILING DATE: 2001-06-22

; PRIOR APPLICATION NUMBER: 09/398,395

; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: 60/130,628

; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: 60/150,262

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 55

; LENGTH: 2861

; TYPE: DNA

; ORGANISM: Abies grandis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (3)...(2606)

; OTHER INFORMATION: abietadiene synthase

US-09-887-586A-55

Query Match 7.0%; Score 194.8; DB 3; Length 2861;

Best Local Similarity 47.8%; Pred. No. 6.8e-40;

Matches 866; Conservative 0; Mismatches 857; Indels 87; Gaps 7;

Qy 337 ATGTAGAAATTTCTGTTCTTCATATGACACAGCATGGGTAGCCATGTCCTTCTCCAA 396

Db 397 ATGGCGAAACGAATCCCTCTGCATATGACACTGCTTGGGTAGCAAGGATCCAGCAGTTG 456

Qy 397 ACTCACCCAAATCGCCTTGTTCCTCGAGTGTCTCAATTTGGTTTAATTAATAATCAGCTTA 456

Db 457 ATGGCTCTGACAAACCTCTACTTCTCTGACAGCGTTGAATGGATTCTTCAAAATCAGTTGA 516

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Qy 637 GTCAACCACTCT---CCCATGTTTGAATCATATTTCTCGTGTGCTGAGTATGCGA 693

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Qy 754 GGGAAATTGGAGCAAAAAAGATGCCATTTCAAATGAGATGGATG-----GATACTTGG 804

Db 799 GGGAGCTAAGCTTAAAGGATTTCCCACTGATGTTCTCTATGCCCTTCCAAACAAACGTTAT 858

Qy 805 CGTATATCTCTCAAGGACTCGGTAAATTTATATATGATTGGAATATGGTGAAGAATATACAGA 864

Db 859 TGTATTTCTTTGGAAGGTTTACAAGAAATAGTAGACTGGCAGAAAAATAATGAACCTTCAAT 918

Qy 865 TGAATAATGGTTCTGTTTTCAACTCACCATCAGCAACAGCTGCTGTTTCAATTAATCATC 924

Db 919 CCAAGGATGGATCAITTTCTCAGCTCTCCGGCATCTACAGCGGCTGTATTTCATGCGTACAG 978

Qy 925 AAAATCCTGGTTGCTTAATATTAATAATCACTTTTGGACAAAGTTTGGTATGCAAGTCC 984

Db 979 GGAACAAAAAGTCTTGGATTTCTTGAACCTTTGCTTGAAGAAATTCGGAACCATGTGC 1038

Qy 985 CAACAGTTTATCTCATGATTTTATTCGACTTTCTATGTTGACACAATTTGAAGAT 1044

Db 1039 CTTGTCACTATCCGCTTGATCTATTTTGAACGTTTGGCGGTTGATACAGTTGAGCGGC 1098

Qy 1045 TAGGAATTTACACCAATTTTCAAGTGGAAATTTAAAAATGTTTTAGATGAAAATACAGAT 1104

Db 1099 TAGGTATCGATCGTCATTTCAAGAGGAGATCAAGGAACATTTGGATTTATGTTACAGCC 1158

Qy 1105 GTTGGGTGGAACGAG-----ATGAGCAAAATATTCATGGATGTTGTAACAT 1149

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Qy 1150 GTGCTTTAGCCTTTCCGTTTATTAAGATCAATGGGTATCAAGTTTCCCGAGATCCATTTGG 1209

Db 1219 CAGCCATGGGCTTCCGAATCTTGAGATTACATGGATACAATGTATCCTCAGATGTTTAA 1278

Qy 1210 CTGAAATTAATAATGAATTTAGCTTTGAAAGACGAATATGACGCTCTTGAACATATCATG 1269

Db 1279 AAACATTTAGATGAGATGGGAGTCTTTTGTCTTGGGTCAACACAGAGAGGAG 1338

Qy 1270 CGTCACATATATTATACC-----AAGAGATTTATCTCTCGAAACAAATCT 1317

Db 1339 TTACAGACATGTTAAACGTCAATCGTTGTTCATGTTTCAITTTCCGGGAGAAACGATCA 1398

Qy 1318 TGAAGTCACTGATTTTC-----CTCAAGAGATAATAT 1350

Db 1399 TGAAGAGAGCAAACTCTGTACGAAAGATATCTGAGGAATGCTCTGGAATAATGTTGATG 1458

Qy 1351 CCACGTATTTCAACAGGCTTTCTTAAATTAATTTCAAAAGAGGTGGAAAAATGCTCTTAAAT 1410

Db 1459 CTTTTCACAAATGGGCTTTTAAAGAAATATTTCCGGGAGAGGTAGAGTATGCATCAAT 1518

Qy 1411 TCCCTATCAATACCGGTTTAGAACGCAATAACACTAGACGAATATACAGCTTTTACAATG 1470

Db 1519 ATCCCTGGCATAGAGTATGCCAAGGTTGGAGGCTAGAAAGCTATATTGAAACATATGGGC 1578

Qy 1471 TAGACATACAGAATTTCTGAAACTACATATCACTCATCAATATTAGTAACTGATTT 1530

Db 1579 CAGATGATGTGGCTTGGAAAACTGTATATATGATGTCATACATTTTCCGATGAAAAAGT 1638

Qy 1531 ACTAAGGTGCTGTTGAAAGATTTCTACACCTGCCAACTATTATTTATCTGTAAGAATAA 1590

Db 1639 ATTTAGAACTAGCAAACTGGACTTCAATAGGTGCACTATACACCAACACAGAGCTTC 1698

Qy 1591 AAGGTCTTGAAGGTGGGTGGTAGAATAAGTTGGACAGCTCAAGTTTGTAGGCAAA 1650

Db 1699 AAGATCTTGAAGGTGGTGAATAATCATCCGTTTTCACCGATCTGAATTTCACTCTGAGC 1758

Qy 1651 AGACCGCTACTGTTATTTCTGTTGCTGCAACCTTTTCGTTCCCGGATTTATCAGATG 1710

Db 1759 GTGTGCGAAATAATATTCTCAACCGCATCTTTTATCTTTGAGCCGAGTTTCTTAAGT 1818

Qy 1711 CGCGTATTTTCAAGGCGCAAAATATGATATTAACATACAGTAGTTGATGATCTTTTGAATA 1770

Db 1819 GCAGAGAGGTTTATACAAAAAATCTTCCAAATTTCACTGTTATTTAGATGATCTTTATGACG 1878

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Qy 1771 TCGTGTGACAAATCGATGAATTTGACCAACCTGATTCATATGTGTTGAAAAATGGAATGTAG 1830
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1879 CCCATGGATCTTTAGACGATCTTAAGTTGTTTCACAGAAATCAGTCAAAGATGGGATCTAT 1938
Qy 1831 ATGTCGACAGGATTTGTTTCAGAGCATGTTTCGGATTTTATTTTATAGCAATAAAGATG 1890
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1939 CACTAG---TGGACCAATGCCACACAAATGAAATATGTTTGTGGGTTTCTACAATA 1995
Qy 1891 CAATCTGTGATTTGGAGATGAAGCTTTTAAATGGCAAGCGCGATGTAAGCCATG 1950
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1996 CTTTATATGATATAGCAAGAGGACGTGAGAGCGAAGGGCGCATGTCTAGGCTACA 2055
Qy 1951 TTATTCAACTGTGTTGGAATCAATGAATAGTATGTTTGAGAGAGCTATATGGAACAAG 2010
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2056 TTCAAAATGTTGGAAGTCCAACTTGAAGCTTACACGAAAGAGAGAGATGGTCTGAAG 2115
Qy 2011 ATGCTTATGTCGAACATTAATGAATATATATGGAAGCGTTAGTGTCAITTTGCAITAG 2070
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2116 CTAATATGTGCCATCTTCAATGAATACATAGAGAAATGCGAGTGTCTCAATAGCATGG 2175
Qy 2071 GCCCGATTGT 2080
Db 2176 GAACAGTCGT 2185
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RESULT 7

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US-09-895-752-55
; Sequence 55: Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-895-752-55
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Query Match 7.0%; Score 194.8; DB 3; Length 2861;
Best Local Similarity 47.8%; Pred. No. 6.8e-40;
Matches 866; Conservative 0; Mismatches 857; Indels 87; Gaps 7;
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Qy 337 ATGTAGAAATTTCTGTTCTTCATATGACACAGCATGGGTAGCCATGGTCCCTTCTCAA 396
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
397 ATGGCGAAACGAATCCCTCTGTCATATGACATGCTGTTGGGTAGCAAGGATTCAGAGCATG 456
Qy 397 ACTCACCAGAAATCCCTTTGTTTCCCTGAGTGTCTCAATTTGGTTAATTAATCAAGCTTA 456
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
457 ATGGCTCTGACAAACCTTCATCTTCTGAGCGGTTGAATGGATTCCTCAAAATCAGTTGA 516
Qy 457 ATGATGGTTTCATGGGGTCTTTGTTAATCACACTCATATCAATATCAATCAATCAATCAAT 516
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
517 AAGATGGGTCTTGGGGTGAAGGATTTCTACTTC-----TTGGCATATG 558
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Qy 517 ATTCTCTATCTTCAACATTAGCATGTATTGTTGCAATTAATAAAGATGGAATGTTTGGGGAAG 576
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559 ACAGATACCTGGCTACACTTGGCATGTATTATACCTTTACCTCTGGCGTACTGGGAGA 618
Qy 577 ATCAATAATAAAGGCTAAAGTTTATTTAGTGAATCAATCTTGTCTTGTCTAGCTACTGAAAA 636
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619 CACAAGTACAGAAAGGTTTGAATTTCTTCAGGACACAAGCTGGAAAGATGGAAGATGAAG 678
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679 CTGATAGTCATAGCCCAAGTGGATTTGAAATAGTATTTTCTGCAATGCTTAAGGAAGCTA 738
Qy 694 AAAAATTTGGACATAAACCTCTTTCAAAAACAAACAGATTTTATGTTGATGCTACATAGA 753
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739 AATCTTAGCTTGGATCTGCTTACGATTTGCCATCTCTGAAACAAATCATCGAANAAGC 798
Qy 754 GGAATTTGGAGCAAAAAGATGCCATTTCAAATGAGATGGATG-----GATACTTGG 804
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799 GGGAGGCTAAGCTTAAAGGATTTCCCACTGATGTTCTATGCCCTTCCAACAACGTTAT 858
Qy 805 CGTATATCTCTGAAGGACTCGGTAAATTTATATGATTTGGAATATGGTGAAGAAATATCAGA 864
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859 TGTATTCTTTGGAAGGTTTACAAGAAATAGTAGCTGGCAGAAATAATGAACTTCAAT 918
Qy 865 TGAATAATGTTCTGTTTCAACTCACCATCAGCAACAGCTGCTGCTTTTCAATTAATCATC 924
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919 CCAAGGATGATCATTTCTCAGCTCTCGGCATCTACAGCGGCTGATATTATGCGGTACAG 978
Qy 925 AAAATCCTGGTGTCTTAATTTAAATTTCACTTTTGGACAAAGTTTGGTAATGCACTGCC 984
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979 GGAACAAAAGTCTTGGATTTCTTGAACCTTGTCTTGAAGAAATTCGGAACCATCTGTC 1038
Qy 985 CAACAGTTTATCTCATGATTTATTTATCCGACTTTCTATGTTGTTGACACAAATTTGAAAGAT 1044
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1039 CTTGTCACTATCCGCTTGATTTTGAACGTTTGTGGCGGTTGATACAGTGTAGCGGC 1098
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1099 TAGGTATCGATGTCATTTCAAGAGGAGATCAAGGAGCATTTGGATTTGTTTACAGCC 1158
Qy 1105 GTTGGGTGGAAACGAG-----ATGAGCAAAATATTATCATGATGTTGTAAACAT 1149
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1159 ATTGGGACGAAAGAGGATTTGGATGGCGAGAGAGAAATCTGTTCTCTGATATTGATGATA 1218
Qy 1150 GTGCTTTAGCCTTTGGTTTAAAGGATCAATGGGTATGAAGTTTCCCGCAGATCCATGG 1209
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1219 CAGCCATGGGCTTCCGAATCTTGAGATTTACATGGATCAATATGATATCTCAGATGTTTAA 1278
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1279 AAACATTTAGAGATGAGATGGGAGTTCTTTTGTCTTCTGGGTCAAAACACAGAGAGAG 1338
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1339 TTACAGACATGTTAAAGCTCAATCGTTGTTTTCATGTTTCCGCGGAGAAACGATCA 1398
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1399 TGGNAGAAGCAAAACCTCTGTACCGAAAGGTATCTGAGGAATGCTCTGGAATAATGGATG 1458
Qy 1351 CCAGTGAATCAACAGGCTTTCTAAATTAATTCACAAAGAGGTGGAAATGCTCTTAAGT 1410
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1459 CCTTGACAAATGGGCTTTTAAAGAGATATTCCGGGAGAGGTAGAGTATGCACTCAAT 1518
Qy 1411 TCCTATCAATACCGGTTTAGAACGACATAAACACTAGACGAAATATATACAGCTTTTACAATG 1470
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1519 ATCCCTGGCATAAGATGATGCCAAGGTTGGAGGTAGAGCTATATTGAAACATCTATGGC 1578
Qy 1471 TAGACAATACAAGAAATTTCTGAAAACTACATATCATCTCAATCAATATTAGTAACACTGAT 1530
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1579 CAGATGATGTGGCTTGGGAAAAAAGTCTATATATGATGCAATCATATTTCCGAATGAAAGT 1638
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Qy	1531	ACCTAAGGTTGGCTGTTGAAGATTTCTACACCTGCCAAATCTATTTATCGTGAAGAAATTA	1590
Db	1639	ATTTAGAACTAGCGAAACTGGAATCTTCAATAAGGTGCAAGTCTATACACCAACACGAGCTTC	1698
	1591	AAGGCTCTTGAAGAGTGGGTGAGAGAAATAGTTGGACCAAGCTCAAGTTTCTGTAGGCAA	1650
Db	1699	AAGATCTTCGAAGGTGTGGAATCATCCGGTTTCACGGAATCTGAATTTTCACTCGTGAGC	1758
Qy	1651	AGACCGCCTACTGTTATTTCTCTGTTGCTGCACAACCTTTCGTCTCCCGAAATTAATCAGATG	1710
Db	1759	GTGTGACGGAATAATATTTCTCACCGGCATCCTTTATCTTTGAGCCCGAGTTTCTTAAGT	1818
Qy	1711	CGGCTATTTCAATGGGCCAAATAATGGGCATATTAACACAGTAGTTGATGACTTTTTTCGATA	1770
Db	1819	GCAGAGAGGTTTATACAAAAAATCTCCAAATTTCACTGTTATTTTAGATGATCTTTTATCAGC	1878
Qy	1771	TCGGTGTGTACAAATCGATGAATTGACCAACCTGATTCGAATGTTTGAAAAATGGAATGTAG	1830
Db	1879	CCCATGGATCTTTAGACGATCTTAAGTTGTTACAGAAATCAGTCAAAAGATGGGATCTAT	1938
Qy	1831	ATGTGCAACAAGGATGTTGTTTCAGAGCATGTTTCGATTTTATTTTAGCATTTAAAGATG	1890
Db	1939	CACTAG---TGGACCAAAATGCCACAACAATGAAATATGTTTGTGGGTTTCTACATA	1995
Qy	1891	CAATCTGTTGGATTTGGAGATGAAGCTTTTAAATGGCAAGCGCGAATGTAACTAGCCATG	1950
Db	1996	CTTTTAATGATATAGCAAAAAGAGGACGTGAGAGGCAAGGCGCGATGTGCTAGGCTACA	2055
Qy	1951	TTATTTCAAACTTCGTTGGAACTAATGATAGTATGTTTGAGAGAGCTATATGACACAGAG	2010
Db	2056	TTCAAAATGTTTGGAAAGTCCAATCTGAAGCTTACACGAAAGACGAGAATGGTCTGAAG	2115
Qy	2011	ATGCTTATGTGCCAAACATTAATGAATATATGAAAAACGGCTTACGTGTCAATTTGCATTAG	2070
Db	2116	CTAAATATGTGCCATCCTTCAATGAATACATAGAGATGCGAGTGTCTCAATAGCATTGG	2175
Qy	2071	GCCCGATTGT	2080
Db	2176	GAACAGTCGT	2185

RESULT 8

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US-09-903-012B-55
; Sequence 55, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph P.
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starko, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-903-012B-55

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Query Match

Query Match

[illegible]


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Db 1399 TGAAGAAGCAAACTCTGTACCGAAAGTATCTGAGAAATGCTCTCGAAATATGCGATG 1458
Qy 1351 CCACGTATCAACAGAGCTTCTAAATTAATTCACAAAGAGGTGGAATGCTCTTAAGT 1410
Db 1459 CTTTGGCAATGGCTTTTAAAGAAATATTCGGGAGAGGTAGATATGCACTCAAT 1518
Qy 1411 TCCCTATCAATACCGGTTTGAACGCAATAACACATAGACGAAATATACAGCTTTTACAATG 1470
Db 1519 ATCCCTGGCATAGAGTATGCAAGGTGGAGGCTAGAGCTATATTTGAAACATATGGGC 1578
Qy 1471 TAGCAATACAGAAATTTCTGAAACTACATATCACTCATCAATATTAATAGTAACACTGATT 1530
Db 1579 CAGATGATGTGGCTTTGGAATACTGTATATATGATGCCATACATATTCGAATGAAAGT 1638
Qy 1531 ACCTAAGGTTGGCTGTTGAAGATTTCTACACCTGCCAATCTATTTATCGTGAAGATTA 1590
Db 1639 ATTTGAACATAGCGAACTGCACTTCAATAGGTGCACTATACACCAACAGAGCTTC 1698
Qy 1591 AAGGCTTTGAAGGTGGGTAGAGAAATAGTTTGGACCAAGTCAAGTTTGTAGGCAAA 1650
Db 1699 AAGATCTTCGAAGGTGGTGAATCATCCGCTTTTACCGGATCTGAAATTCACCTGCGAGC 1758
Qy 1651 AGACCGCTACTGTTATTTCTGTTGCTGCTGCAACACTTTTGTCTCCGAAATATACAGATG 1710
Db 1759 GTGTGACGGAATATATTTCTCACCGCATCTTTATCTTTGAGCCGAGTTTTCTAAGT 1818
Qy 1711 CGGTATTTCTATGGCCCAAAATGGCATATTAACATACAGTAGTTGATGACTTTTTCGATA 1770
Db 1819 GCAGAGAGTTTATACAAAACTTCCAAATTTCACTGTTATTTTAGATGATCTTTATGACG 1878
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Db 1879 CCAATGATCTTTAGACGATCTTAAAGTTGTTTACAGAACTAGTCAAAAGATGGATCTAT 1938
Qy 1831 ATGTGCAAGAGATGTTGTTTGTGAGAGCATGTGCGATTTTATTTTAGCAATTAAGAGATG 1890
Db 1939 CACTAG---TGGACCAATGCCAACAAATGAAATATGTTTGTGGGTTTCTACAATA 1995
Qy 1891 CAATCTGTTGATGGAGATGAGCTTTTAAATGGCAAGCGCGATGTAAGTACTAGCCATG 1950
Db 1996 CTTTTAATGATATAGCAAAAGAGGACGTGAGGCGCAAGCGCGATGTCGTAGGCTACA 2055
Qy 1951 TTAATTCAACTGTTGGAACATATGAATAGTATGTTGAGAGAGCTATATGGACAAAG 2010
Db 2056 TTCAAAATGTTGGAAGTCCAACTTGAAGCTTACACGAAGAGAGAGATGTTCTGAAG 2115
Qy 2011 ATGCTTATGTCCAACAAATTAATGAATATATGGAAGAAACGCTTACGTGCTATTTGCAATAG 2070
Db 2116 CTAATATGTGCCATCCTTCAATGAATACATAGAGATGCGAGTGTGTCAATAGCATTTG 2175
Qy 2071 GCGCGATTGT 2080
Db 2176 GAACAGTCGT 2185

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RESULT 9

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US-09-900-797-55
; Sequence 55, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6645762, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262

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; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-900-797-55

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Query Match 7.0%; Score 194.8; DB 3; Length 2861;
Best Local Similarity 47.8%; Pred. No. 6.8e-40;
Matches 866; Conservative 0; Mismatches 857; Indels 87; Gaps 7;

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Qy 337 ATGTAGAAATTTCTGTTTCTTCATATGACACAGATGGGTAGCCATGGTCCCTTCTCAA 396
Db 397 ATGCGAAACGAATCCCTCTGCATATGACACTGCTTGGGTAGCAAGGATTCAGCAGTTG 456
Qy 397 ACTCACCCCAATCGCCTTGTTCCTGAGTGTCTCAATTCGTTAATTAATTAACAGCTTA 456
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Qy 457 ATGATGGTTTCATGGGGTCTTGTAAATCACAATCAATAATACCCCGTTCCTTAAAG 516
Db 517 AAGTGGTCTTGGGGTGAAGGATTCCTACTTC-----TTGGCATATG 558
Qy 517 ATTCTCTATCTCAACATTAGCATGATTTGTTGCATTTAAAGAGATGGAATGTTGGGGAAG 576
Db 559 ACAGAACTACTGGCTACACTTGCATGATTTATTAACCTTACCTCTGGCGTACTGGGAGA 618
Qy 577 ATCAATAAATAAGTCTAAGTTTATTCAGTCAATCTTGTCTTGTGCTTGTGCTACTGAAAA 636
Db 619 CACAGTACAGAAAGGATTTGAATTTCTTCAAGSACACAGCTGGAAGATGGAAGATGAAG 678
Qy 637 GTCAACCATCT---CCATTTGGTTTGAACATATATTTCTGTTTGTCTTGTGATATGCGA 693
Db 679 CTGATAGTCAATAGCCCAAGTGGATTTGAATAGTATTTCTGCAATGCTAAGGAAGCTA 738
Qy 694 AAAAATTGGACATPAACCTCTTCAAAACAAACAGATTTTGTGATGATGCTACATAGA 753
Db 739 AAATCTTAGCTTGGATCTGCTTACGATTTGCAATTTCTTGAACAAATCATCGAAAGC 798
Qy 754 GGAATTTGGAGCAAAAGATGCCATTCATATGAGATGAGT-----GATCTTGG 804
Db 799 GGGAGGCTAAGCTTAAAGGATTTCCCACTGATGTTCTTATGCCCCTTCCAAACACGTTAT 858
Qy 805 CGTATATCTCTGAAGGACTCGGTAATTTATATGATTTGGAATATGTTGGAAGATATCAGA 864
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Qy 1105 GTTGGGTGGAAACGAG-----ATGAGCAAAATATTCATGATGTTGTACAT 1149
Db 1159 ATTGGGACGAAAGAGGCAATTTGGATGGCGGAGAGAAATCCTGTTCTCTGATATTTGATGATA 1218

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Qy 449 TCAGCTTAATGATGGTTCAATGGGCTTTGTTAAATCACATCATATCATATCACCGGTT 508
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Qy 509 GCTTAAAGATTCTCTATCTTCAACATTAAGCATGATGTTGTCATTAAGAGATGGAATGT 568
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Qy 1255 -TTGAACATATCATGCTGCATATATATACCAAG- -GGATTATCTTCTGGAAC 1311
Db 1353 ATTGAGAAGCGTGGTGAATCTTTTTCAGAGCTTCCGACCTTCCGATTTCCGACGAAGAGC 1412
Qy 1312 AAATCTTTGAAGTCAAGTATTTCTTCAAGAGATAATATCCACTGATTTCAAAACAGGCTTT 1371
Db 1413 TATGAGCATGCTAGAAAATTTGAGAACCATATCTTAGAGAGGCACTTGCACGAAAT 1472
Qy 1372 CTAATTAATTTCA- -CAAAGAGTGGAAAATGCTCTTTAAGTTTCCCTATCAATAC 1423
Db 1473 CTCAACCAATACAAAATTAATTTCAAGAGATTTAGTACGTTGGTGGAGTACCTTTGGCACAT 1532
Qy 1424 CGGTTTAGACGCAATAACACTAGACCAATATACAGCTTTACATGTTAGACATACAG 1483
Db 1533 GAGTATCCCAAGCTTAGAGCCGAAGTTTATTTGATTTATATGACGACAAATTTATGATG 1592
Qy 1484 AATTCTGAAAACATACATATCACTCATCAATATTTAGTAAACACTGATTACCTAAGTTTGGC 1543

Db 1593 GCAGAGGAAGACTCTATATAGAATGCCATCTTTGAGTAAATTTCAAAATGTTTGAATTTGGC 1652
Qy 1544 TGTGAAGATTCTTACACCTGCCAATCTATTTATTCGTGAAGAAATTTAAAGGCTCTTGAAG 1603
Db 1653 AAAATTGGACTCTCAATATCGTACAACTTTTGCATCAAGAGGAGTTGAAGCTTTCAACAAG 1712
Qy 1604 GTGGTGGTGAAGAAATAAGTTGGACCACTCTTCTGCTCCCGAAATTTACAGATCGGCGTACTG 1663
Db 1713 ATGGTGAAGAAATCCGGATGGCAGATATAAATTTCACTCGACACCGAGTGGCGAGGT 1772
Qy 1664 TTAATTTCTGTTGCTGCAACACTTTCTGCTCCCGAAATTTACAGATCGGCGTATTTTCATG 1723
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Qy 1784 CGATGAATTCACCAACCTGATTTCAATGTTTGAAGAAATGGAATGTAGATGTCGACAAGGA 1843
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Db 2004 AAATAATGATGTTGTTTAAAGTCAAGGACGTCATGCTCGCTCACATAAGAAACCCCTG 2063
Qy 1964 GTTGGAACTAATGAATGATGTTGAGAGAGCTTATATGACAAAGAGATGCTTATGTGCC 2023
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Db 2364 TAATCCAGGAGCAACTGAGGAAGATGCCATTAAGCACAT 2402

RESULT 13

US-09-398-395A-43
; Sequence 43, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6468772, Joseph P.
; APPLICANT: Sparks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCES: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22

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; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Taxus brevifolia
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)...(2607)
; OTHER INFORMATION: taxadiene synthase
US-09-398-395A-43

Query Match      5.5%; Score 153.8; DB 3; Length 2700;
Best Local Similarity 46.7%; Pred. No. 2.5e-29;
Matches 943; Conservative 0; Mismatches 992; Indels 84; Gaps 11;

QY 335 AAATGTAGAAATTCCTGTTCTTCATATGACACAGCATGGTAGCCATGGT-----CCC 388
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QY 1043 ATTAGGAATTTACACCATTTTCAGATGGAATTAATAATTTTATGATGAACATACATAC 1102
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QY 1103 ATGTTGGGTGGAACGAG-----ATGAGCAAAATATTCATGGATGTTGTAAC 1147
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DB 1773 TTTATTTTTCATCAGCTACA-----TTTGAACCCGAAATATCTGCGACCTAGAAATTTGCC 1826
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DB 1947 ---GATTCAGAGTGTATGCAAACTTGTCTTTAAAGTTTGGTTCAAAATTTGAAGAAGT 2003
QY 1904 TGGAGATGAAGCTTTTAAATGGAAGCGCGATGTAACTAGCCATGTTTATTTCAAACTTG 1963
DB 2004 AAATGAATGATGTTTGAAGTACAGAGCGTGCATGCTGCTCACAATGAAGAAACCTTG 2063
QY 1964 GTTGAACCTTAATGAATAGTATGTTGAGAGAACTATATGGAACAAGAGATGCTTTATGTC 2023
DB 2064 GGAGTTGACTTCAATTTGTTATGTACAAGAAAGGAGTGGCTTGAAGCGGGTATATATACC 2123
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DB 2124 AACTTTTGAAGAGTACTTTAAAGACTTTATGCTATATCAGTAGGCTTTGAGCCGCTGATACC 2183
QY 2084 GCGGCTATTTACTTTTGTGGGCCCAAAATTTATCAGAGGAGATTTGTTGAAGCTCTCAATA 2143
DB 2184 ACAACCAATCTACTAATGGGTGAGCTTGTGAAAGATGATGTTTGTGAGAAAGTGACTA 2243
QY 2144 TC---ATAATCTATTAAAGCTAATGAGCAGCGAGGCTCGACTTCTTAAACGATATTCATAG 2200
DB 2244 TCCCTCAATAATGTTTGTAGCTTGTATCTTTGAGCTGGCGACTAAACAAAGCAGACCAAAAC 2303

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Db 1887 AGATGAATGAAAAGTTTCACTCAGGGAGTAAGAGATGGGATACATCTTTTGTCTACATGA 1946
QY 1844 TTGTTGTTCAGAGCATGTTTGGGATTTTATTTTATGCAATTAAGAGATGCAATCTGTTGGAT 1903
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QY 1904 TGGAGATGAAGCTTTTAAATGGCAGCGCGCATGTAACTAGCCATGTTTATTCAAACTTGG 1963
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RESULT 15

US-09-895-752-43
; Sequence 43, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASE
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Taxus brevifolia
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)...(2607)
; OTHER INFORMATION: taxadiene synthase
US-09-895-752-43

Query Match 5.5%; Score 153.8; DB 3; Length 2700;
Best Local Similarity 46.7%; Pred. No. 2.5e-29;
Matches 943; Conservative 0; Mismatches 992; Indels 84; Gaps 11;
QY 335 AAATGTAGAAATTTCTGTTCTTCATATGACACAGCATGGTAGCCATGCT-----CCC 388

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Job time : 501.49 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 08:16:57 ; Search time 249.08 Seconds

(without alignments)

2854.981 Million cell updates/sec

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Perfect score: 1720

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Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:
9: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:
10: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:
11: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:
12: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:
13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	240	14.0	975	12	US-11-098-686-9415 Sequence 9415, Ap
2	240	14.0	1457619	12	US-11-098-686-8739 Sequence 8739, Ap
3	236	13.7	972	8	US-10-467-657-279 Sequence 279, App
4	236	13.7	972	8	US-10-467-657-4381 Sequence 4381, Ap

c	5	236	13.7	972	8	US-10-467-657-8261	Sequence 8261, Ap
	6	204	11.9	2987	12	US-11-194-246-99	Sequence 99, Appl
	7	189.5	11.0	948	12	US-11-119-351-5	Sequence 5, Appli
	8	174.5	10.1	960	8	US-10-793-626-1039	Sequence 1039, Ap
	9	174.5	10.1	2317	8	US-10-793-626-4357	Sequence 4357, Ap
	10	174.5	10.1	2987	8	US-10-793-626-3398	Sequence 3398, Ap
	11	164.5	9.6	903	12	US-11-098-686-9307	Sequence 9307, Ap
	12	164	9.5	888	12	US-11-194-246-139	Sequence 139, Ap
	13	164	9.5	2885	12	US-11-194-246-94	Sequence 94, Appl
	14	159	9.2	3444	8	US-10-793-626-4144	Sequence 4144, Ap
c	15	159	9.2	4045	8	US-10-793-626-3929	Sequence 3929, Ap
	16	155	9.0	966	12	US-11-092-140-11	Sequence 11, Appl
	17	152	8.8	1101	7	US-10-524-972-113	Sequence 113, Appl
	18	152	8.8	1101	8	US-10-524-972-125	Sequence 125, Appl
	19	150	8.7	1402	7	US-10-524-972-109	Sequence 109, Appl
	20	150	8.7	1402	8	US-10-524-972-121	Sequence 121, Appl
	21	147.5	8.6	1116	8	US-10-467-657-6749	Sequence 6749, Ap
	22	145.5	8.5	783	8	US-10-793-626-223	Sequence 223, Appl
	23	145	8.4	5632	12	US-11-070-080-6	Sequence 6, Appli
	24	145	8.4	8814	12	US-11-070-080-41	Sequence 41, Appl
	25	144.5	8.4	561	12	US-11-092-140-10	Sequence 10, Appl
	26	139.5	8.1	888	12	US-11-129-143-184	Sequence 184, Appl
	27	138.5	8.1	888	8	US-10-967-671-1	Sequence 1, Appli
	28	138.5	8.1	888	8	US-10-967-671-3	Sequence 3, Appli
	29	135	7.8	1612	12	US-11-129-143-157	Sequence 157, Appl
c	30	134.5	7.8	2130	12	US-11-194-246-373	Sequence 373, Appl
c	31	134.5	7.8	2255	12	US-11-194-246-129	Sequence 129, Appl
	32	125.5	7.3	894	8	US-10-467-657-2849	Sequence 2849, Ap
	33	125.5	7.3	894	8	US-10-467-657-6749	Sequence 6749, Ap
	34	125	7.3	1155	7	US-10-524-972-111	Sequence 111, Appl
	35	125	7.3	1155	8	US-10-524-972-123	Sequence 123, Appl
	36	120.5	7.0	1087	12	US-11-092-140-15	Sequence 15, Appl
	37	112	6.5	950	12	US-11-070-080-35	Sequence 35, Appl
c	38	109.5	6.4	2872	8	US-10-240-708-91	Sequence 91, Appl
c	39	105.5	6.1	4434	12	US-11-140-930-16	Sequence 16, Appl
	40	103	6.0	3021	8	US-10-793-626-153	Sequence 153, Appl
	41	101	5.9	200	12	US-11-098-686-4594	Sequence 4594, Ap
c	42	101	5.9	1790	12	US-11-136-527-2252	Sequence 2252, Ap
c	43	97.5	5.7	1481	8	US-10-750-185-29175	Sequence 29175, A
c	44	97.5	5.7	1481	8	US-10-750-623-29175	Sequence 29175, A
c	45	95.5	5.6	981	12	US-11-092-140-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-11-098-686-9415
; Sequence 9415, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9415
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-11-098-686-9415

Alignment Scores:
Pred. No.: 2.47e-16 Length: 975
Score: 240.00 Matches: 90
Percent Similarity: 44.6% Conservative: 50
Best Local Similarity: 28.7% Mismatches: 125


```
QY 231 GluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGlyGln 250
Db 631482 GAAGGCAAAATTACACCACTTTTATAC-----TATTTAAACA----- 631523
QY 251 ThrGluGlnHisAsnGluLeuLeuArgIleLeuLeuLeuArgThrSerAspLysAspIle 270
Db 631524 -----CTTTCTTTAGAGAAATAATAATA 631547
QY 271 LysLeuLysLeuIleGlnIleLeuGluPhe---AspThrAsnSerLeuAlaTyThrLys 289
Db 631548 TTTATAAAAAAATTTCAACTCATCTTTACAGATGAAGATACCTATTATTACCAGG 631607
QY 290 AsnPheIleAsnGlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyLeuPro 309
Db 631608 GTCATCCATCAACAAATTTTGATCAAAAAACACGGGAATTAGCAATGTTTATTTCAA 631667
QY 310 AspLeuAlaSerHisSerAspThrAlaThrAsnLeu 321
Db 631668 AAAGCTTTTAAACAATTTAGAAATTATTAACTAATGTT 631703

RESULT 3
US-10-467-657-279
; Sequence 279, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 279
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-279

Alignment Scores:
Pred. No.: 6.8e-16 Length: 972
Score: 236.00 Matches: 66
Percent Similarity: 48.8% Conservative: 61
Best Local Similarity: 25.4% Mismatches: 109
Query Match: 13.7% Indels: 24
DB: 8 Gaps: 6

US-10-041-018-22 (1-335) x US-10-467-657-279 (1-972)
QY 3 AlalysileAspGluLeuIleAsnAsnAspProValTrpSerSerGlnAsnGlu---Ser 21
Db 49 GCCAAGTCAATGAAGTCATCAACCGT-----CGGTGCAATCCGATGTCGCA 96
QY 22 LeuIleSerLysProTyAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeuAsn 41
Db 97 CTGATTTCCGAAATCGGTACATATATCATCAGCGCGGCGCAAAACGCTCGCTCCGATT 156
QY 42 LeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleValSer 61
Db 157 ATGACGATTTTGGCGGGTAGGCGGTGTTATGATCAGCAAACTGTATTCTCGTGGCA 216
QY 62 GlnIleValGluLeuLeuIleAsnSerSerLeuIleAspAspIleGluAsnAla 81
Db 217 GCGATGTCAGTTATTCACACTTCACACTCTCGACACGATGTCGATGAAGC 276
QY 82 ProLeuArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsn 101
Db 277 GATTTGGCGGTCGGCGCAACGGCAACAATCTGTTCGCAATGCGCGGCGAGTGTG 336
```

```
QY 102 ThrAlaAsnTyMetTyPheArgAlaMetGlnLeuVal-----SerGlnLeuThr 118
Db 337 GTTGGCGACTTTTATATATACCGGTGCATTTCACTGATGTTGCTCGGCAGTATCGGC 396
QY 119 ThrLysGluProLeuTyHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeu 138
Db 397 GTTTTGGAGTGTATGCGGATCGGACCAACATCATTTCCCGGAGGAGGTCATCGAGTGT 456
QY 139 HisArgGlyGlnGluLeuAspIleTyTrpArgAspPheLeuProGluIleIleProThr 158
Db 457 ATGAACATCGGCAATACGGACATT-----ACC 483
QY 159 GlnGluMetTyLeuAsnMetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeu 178
Db 484 GAAGAACATATATCCGATCATCCATATAAAACGGCAAAATGTTTGAAGTCGCGCT 543
QY 179 ArgLeuMetGluAlaLeuSerProSerSer---HisHisGlyHisSerLeuValProPhe 197
Db 544 CAAATCGCGCAATTTTGGGCAAAAGCTTCCCGCGGCACGAACAGGCTTTGAAAGACTAC 603
QY 198 IleAsnLeuLeuGlyIleIleTyGlnIleArgAspAspTyTrpLeuAsnLeuLysAspPhe 217
Db 604 GGTATGTACGTGCGGTACGGCATTTCCAGATTATTGACGATGCTGCGATTATTCGGGGAA 663
QY 218 GlnMetSerSerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPhePro 237
Db 664 ACCGAGAAACAGGTAAACAGTCGCGGACGATTTGCGGAGGAGGAAACCGACCTCGCT 723
QY 238 IleValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIle 257
Db 724 TTGATTTATCTGATGCGT-----CAGGGTTCCGAACAGGTTGCGAACGATGTG 771

RESULT 4
US-10-467-657-4381
; Sequence 4381, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4381
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4381

Alignment Scores:
Pred. No.: 6.8e-16 Length: 972
Score: 236.00 Matches: 66
Percent Similarity: 48.8% Conservative: 61
Best Local Similarity: 25.4% Mismatches: 109
Query Match: 13.7% Indels: 24
DB: 8 Gaps: 6

US-10-041-018-22 (1-335) x US-10-467-657-4381 (1-972)
QY 3 AlalysileAspGluLeuIleAsnAsnAspProValTrpSerSerGlnAsnGlu---Ser 21
Db 49 GCCAAGTCAATGAAGTCATCAACCGT-----CGGTGCAATCCGATGTCGCA 96
QY 22 LeuIleSerLysProTyAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeuAsn 41
Db 277 GATTTGGCGGTCGGCGCAACGGCAACAATCTGTTCGCAATGCGCGGCGAGTGTG 336
```

```
Db 97 CTGATTTCCGAATCGGTACATATATCATCAGCGCGGGCGGCAAAACGCGTGGTCCGATT 156
Qy 42 LeuileValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleValSer 61
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 157 ATGACGATTTGGCGGGTAAGCGGTCCGGTTATGATGACGAGAAACTGTATTCTGCTGGCA 216
Qy 62 GlnIleValGlnLeuLeuHisAsnSerSerLeuLeuLeuLeuLeuLeuLeuLeuLeu 81
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 217 GCGATGGTGGAGTTTATCCACACTTCCACACTCTTCGCGCAATCTGCGCGGCGCAGTTG 276
Qy 82 ProLeuArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsn 101
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 277 GATTTGGCGCGTGGCGGCAACGCAACATCTGTCGCAATCGCGCGGCGCAGTTG 336
Qy 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuVal-----SerGlnLeuThr 118
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 337 GTTGGCGACTTTTATATATACCGGTGCAATTCAACTGATGGTTGCCGCGCAGTATGCCG 396
Qy 119 ThrLysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuLeuLeu 138
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 397 GTTTTGGAAAGTATGCGCGGATCGACCAACATCATTTGCCGAGGAGAGGTCTATGCAGCTG 456
Qy 139 HisArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThr 158
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 457 ATGAACATCGGCATACGACATT-----ACC 483
Qy 159 GlnGluMetTyrLeuAsnMetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeu 178
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 484 GAAGAACAATATATCCGAGTCATCCAAATATAAAACGGCAAAATTTGTTGAAGCTGCCGCT 543
Qy 179 ArgLeuMetGluAlaLeuSerProSerSer---HisHisGlyHisSerLeuValProPhe 197
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 544 CAAGTCGGCGCAATTTTGGGCAAGCTTCCCGGGCACGAACAGGCCCTTGAAGACTAC 603
Qy 198 IleAsnLeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPhe 217
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 604 GGTATGCTCGTACGCGCATTCAGATATGACATGCTGCTGATTTATTCGGGGGAA 663
Qy 218 GlnMetSerSerGlyGlyPheAlaGluAspIleThrGlyLysLeuSerPhePro 237
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 664 ACCGAAGAAACAGGTAAAAACGTCGCGCAGCATTTGGCGGAAGGAAACCGACCTGCCT 723
Qy 238 IleValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIle 257
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 724 TTGATTTATCTGATCGGT-----CAGGGTTCCGAACAGGTTCCGAACGATGTG 771
```

RESULT 5

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US-10-467-657-8261/c
; Sequence 8261, Application US/10467657
; Publication No. US20050260591A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8261
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8261
```

Alignment Scores: 6.8e-16 Length: 972
Pred. No.: 236.00 Matches: 66
Score:

```
Percent Similarity: 48.8% Conservative: 61
Best Local Similarity: 25.4% Mismatches: 109
Query Match: 13.7% Indels: 24
DB: 8 Gaps: 6
US-10-041-018-22 (1-335) x US-10-467-657-8261 (1-972)
```

```
Qy 3 AlaLysIleAspGluLeuIleAsnAsnAspProValTrpSerSerGlnAsnGlu---Ser 21
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 924 GCCAAGTCAATGAAGTCATCAACCGT-----GCCGTGCAATCCCATGTGCGCA 877
Qy 22 LeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeuAsn 41
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 876 CTGATTTCCGAATCGGTACATATATCATCAGCGCGGCGGCAAAACGCTGGTCCGATT 817
Qy 42 LeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleValSer 61
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 816 ATGACGATTTTGGCGGTAAGCGGTCCGGTTATGATGACGAGAAACTGTATTCTGCTGGCA 757
Qy 62 GlnIleValGluLeuLeuHisAsnSerSerLeuLeuLeuLeuLeuLeuLeuLeuLeu 81
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 756 GCGATGGTGGAGTTTATCCACACTTCCACACTCTTCGACGACGATGTCGTCGATGAAGC 697
Qy 82 ProLeuArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsn 101
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 696 GATTTGGCGCGTGGCGGCAACGCAACAACTGTTTCGGCAATCGCGCGCAGTGTG 637
Qy 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuVal-----SerGlnLeuThr 118
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 636 GTTGGCGACTTTTATATATACCGGTGCAATTCAACTGATGGTTGCCGCGCAGTATGCGC 577
Qy 119 ThrLysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuLeuLeu 138
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 576 GTTTTGGAAAGTATGCGCGGATCGACCAACATCATTTGCCGAGGAGAGGTCTATGCAGCTG 517
Qy 139 HisArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThr 158
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 516 ATGAACATCGGCATACGACATT-----ACC 490
Qy 159 GlnGluMetTyrLeuAsnMetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeu 178
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 489 GAAGAACAATATATCCGAGTCATCCAAATATAAAACGGCAAAATTTGTTGAAGCTGCCGCT 430
Qy 179 ArgLeuMetGluAlaLeuSerProSerSer---HisHisGlyHisSerLeuValProPhe 197
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 429 CAAGTCGGCGCAATTTTGGGCAAGCTTCCCGCGCACGAACAGGCCCTTGAAGACTAC 370
Qy 198 IleAsnLeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPhe 217
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 369 GGTATGTCGTCGGTACGCGCATTCAGATATGACATGCTGCTGATTTATTCGGGGGAA 310
Qy 218 GlnMetSerSerGlyGlyPheAlaGluAspIleThrGlyLysLeuSerPhePro 237
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 309 ACCGAAGAAACAGGTAAAAACGTCGCGCAGCATTTGGCGGAAGGAAACCGACCTGCCT 250
Qy 238 IleValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIle 257
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 249 TTGATTTATCTGATCGGT-----CAGGGTTCCGAACAGGTTCCGAACGATGTG 202
```

RESULT 6

```
US-11-194-246-99
; Sequence 99, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND METI
; FILE REFERENCE: 00592.US1 (MER 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
```



```
QY 145 AspileTyrTrpArgaspPheLeuProGluIlelleProThrGlnGluMetTyrLeuAen 164
DB 418 CAGATGGTCGTGCAGAAC-----GACCTTACGACCGCTGTAGACGCTATCTTGAA 468
QY 165 MetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeuArgLeu-----MetGlu 182
DB 469 GTCATTACCGGCMAGACGCTGGCTGTTTGGCGTCCCTGGCGTCCGCGCTGTCGTG 528
QY 183 AlaLeuSerProSerHisHisGlyHisSerLeuValProPheIleAsnLeuGly 202
DB 529 GCGAGCGTCGGAACGACGAAGAG---GAAGCTCTGGAGCGGTTTGGCACCAATCTGGGT 585
QY 203 IleIleTyrGlnIleArgaspPheTyrLeuAsnLeuLysAspPheGlnMetSerSerGlu 222
DB 586 ATGGCGTTCAGCGTTTGTGATGATGCTGCTGGAACCTGATATGCGCGACACGAGCGGTTTGGGC 645
QY 223 LysGlyPheAlaGluaspIleThrGluGlyLysLeuSerPheProIleVal----- 239
DB 646 AAGACGTTGGTGATGACATGCGTGAAGGACAGATCACCCTGCGCGTCTGCGCGCTAT 705
QY 239 ----- 239
DB 706 GAGGCTGGCTCGCGGAAGATCGTATTTCTGGAGCGCGTCATTGGAGAGGGGAGCAG 765
QY 240 -----HisAlaLeuAsnPheThrLysThrLysGly----- 249
DB 766 ACTGAGGACGATCTGCTCCTCATGCTCTGAACCTGATTCGAAAGACGCGTCCGATCAATACG 825
QY 250 -----GlnThrGluGlnHisAsnGluIleLeuArgIleLeuLeu 262
DB 826 AGATCGCGCGCGGAGGTCTATGCGGACGCGAGCTGTTGAAGCCCTGTCATTTTC----- 882
QY 263 LeuArgThrSexAspLysAspLysLeuLysLeuLeuGlnIleLeuGluPheAspThr 282
DB 883 -----CCGATACGACGACGCGCGCTCTGATCGAAACGGTTCAGTTCACGGTG 933
QY 283 Asn 283
DB 934 AAT 936
```

RESULT 8

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US-10-793-626-1039
; Sequence 1039, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1039
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-1039
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Alignment Scores:
Pred. No.: 3,98e-09 Length: 960
Score: 174.50 Matches: 74
Percent Similarity: 42.9% Conservative: 70
Best Local Similarity: 22.0% Mismatches: 131
Query Match: 10.1% Indels: 61
DB: 8 Gaps: 13
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US-10-041-018-22 (1-335) x US-10-793-626-1039 (1-960)

```
QY 3 AlaIlelleAspGluLeuIleAsnAsp-----ProValTrpSerSerGlnAsnGlu 20
DB 4 GCAAGATTAAAC-----ATTAAACACGAATAAAGAAAGTAGAAAGCGACTTGAAGAA 57
QY 21 SerLeuIleSerLysProTyrAsn-----HisIleLeuLeuLysPro 34
DB 58 GCAATTATAAGTTCGATCAAAACATTACAAGAGCGCTCATTCATTTACTATCTTCAGGG 117
QY 35 GlyLysAsnPheArgLeuAsnLeuIleValGlnIleAsnArgVal-----MetAsnLeu 52
DB 118 GGAATAAGAGAGTTAGACCCGCTTTTGTATTATTAAAGTGGTCAATTTGGCTCTAACACAAA 177
QY 53 ProLysAspGlnLeuAlaIleValSerGlnIleValGluLeuLeuHisAsnSerSerLeu 72
DB 178 CCTTCAGAGACACCGTATCGTGCAGTAGCTTTAGAACTAATTCCACATGGCTACTCTTA 237
QY 73 LeuIleAspAspIleGluAsnAlaProLeuArgArgGlyGlnThrThrSerHisLeu 92
DB 238 GTCCAGATGATGTAGATAGATAAAGTAGTAACAGTAGAGCGGCGACTCACTATTTCAAA 297
QY 93 IlePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGln 112
DB 298 AATGGGACCAAGTAGACGTATTTTAAACAGGAAATTTCTTACTTGCTATGGGCTCAAG 357
QY 113 LeuValSerGlnLeuThrThrLysGluProLeuTyrHisAsnLeuIleThrIlePheAsn 132
DB 358 CATTTATCTGAATCAGT-----GATACCTGTCCTCATTCGACCAAT-----TCT 402
QY 133 GluGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeu 152
DB 403 AATCAATTTGTGTGTGTGTAGAGGAGAACTATTC-----CAATTTCAA 447
QY 153 ProGluIleIleProThrGlnGluMet-----TyrLeuAsnMetValMetAsnLysThr 170
DB 448 GATCAATTTAATAGCAATCAAACAATTACTAATTTACTTACGTGCTAATCAACCGTAAACA 507
QY 171 GlyGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerHisHis 190
DB 508 GCACCTCTTATTCAACTGTCTACAAAGTGTGTGCGAATTACTTCCAAATCGCTCAAAATGAC 567
QY 191 -----GlyHisSerLeuValProPheIleAsnLeuGly 202
DB 568 GTATTTCGTAAATTAATAATGATCGACAT-----TATATAGGT 606
QY 203 IleIleTyrGlnIleArgaspPheTyrLeuAsnLeuLysAspPheGlnMetSerSerGlu 222
DB 607 ATGAGTTTCCAAATAATAGATGATGCTAGATTTTACTAGTTCTGAAAGAAACTTGGT 666
QY 223 LysGlyPheAlaGluaspIleThrGluGlyLysLeuSerPheProIleValHisAlaLeu 242
DB 667 AAGCCGGTTGGTAGTGACCTTATGAATGGCTATATACATTACCTCTACTATTAGAATG 726
QY 243 AsnPheThrLysThr-----LysGlyGlnThrGluGlnHis 254
DB 727 CGAAAAAATAAGACTTTTAAAGATAAAATTTCAACATTAATCCTCACAGCTCTCAACAT 786
QY 255 AsnGluIleLeuArgIleLeuLeuArgThrSerAspLysAspLysLeuLysLeu 274
DB 787 GCCTTTGAAACTTGTATATAAATAATTAGACAGTCCGAAAGCATAGAACAAATCAAAACAA 846
QY 275 IleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGln 294
DB 847 ATA-----AGTGAAAGTATTATAATAA 870
QY 295 LeuValAsnMetIleLys-----AsnAspAsnGluAsnLysTyrLeu 308
DB 871 GCAATCAATTTAATCGATCAATTAGAGGATGGTCTCTAATAAAGAACTA 918
```

RESULT 9

```
US-10-793-626-4357
; Sequence 4357, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
```

```

Db      1488   ... :... ||||| ||||| ||||| ||||| |::| ::| |::| ::|
Qy      223     LysGlyPheAlaGluAspIleThrGluGlyLeuSerPheProIleValHisAlaLeu    242
Db      1548   AAGCCGGTGTAGTGACCTTTATGAATGGTCATTACTACTGTACTATTAGAATG    1607
Qy      243   AsnPhethrLysThr-----lysGlyInthrGluGlnHis    254
Db      1608   CGAAAAAATAAGAACTTTTTTAAGATAAAAATTTCAACAATTAATCGTAGCAGCTCCTCAACAT    1667
Qy      255   AsnGluileLeuargilleLeuLeuLeuArgThrSerAspIysAspileYsLeuYsLeu    274
Db      1668   GCCTTTGAAACTGTATACAATAATTAGACAGTCGAAAGCATAGAACCAATCAAACAA    1727
Qy      275   IleGlnileLeuGluPheAspThrsenSerLeualaTyThrLysasnPheIIeAsnGln    294
Db      1728   ATA-----AGTGAAAAGTATTAAATAAA    1751
Qy      295   LeuValasnMetilellys-----AsnAspAsnGluasnlYSTyrLeu    308
Db      1752   GCAATCAATTTAATCGATGAATTAGAGGATGGTCCTTAATAAGAACTTA    1799

RESULT 10
US-10-793-626-3398
; Sequence 3398, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3398
; LENGTH: 2987
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3398

Alignment Scores:
Pred. No.:          1,72e+08        Length:         2987
Score:             174.50           Matches:            74
Percent Similarity: 42.9%           Conservative:       70
Best Local Similarity: 22.0%        Mismatches:       131
Query Match:       10.1%           Indels:            61
DB:                8               Gaps:              13

US-10-041-018-22 (1-335) x US-10-793-626-3398 (1-2987)
Qy      3     AlaValIleaspGlulelleAsnAsnAp-----ProValTrpSerSerGlnAsnglu    20
Db      885   GCAAGTTAANC-----ATTACAAGAAATAAAGAAAGTAGAAAAGCACGACTTGAGAA    938
Qy      21     SerLeulleSerLysProfYrAsn-----HistleLeuLeuLyspro    34
Db      939   GCAATTATAAGTTCTGATCAACAATTAACAAGAGGCCTCATTGCCATTACTTCTTCAGGG    998
Qy      35     GlyLyvAsnPheArgeutaeNLeuilleValGlnIleAsnArgVal-----MetAsnLeu    52
Db      999   GGAAAAAGAGTTAGACCCTGCTTTTGTATTATTTTAAGTGGTCCAATTTGGCTCTTAACAACAAA    1058
Qy      53     ProLyvaspGlnLeualalIleValserGlnIlevalGluLeuHisAsnSerSerLeu    72
Db      1059   CCTTCAGAGACACAGGTATCGGTGACGATGAGCTTTTAGAATCAATTAATCATGGTGCCTTA    1118
Qy      73     LeuilleAspAspileGluAspAsnAlaProLeuarGArgglyGlnThrThrSerHisLeu    92
```

```
Db 1119 GTCCAGATGATGATAGATAAAGATGATGAACCGTAGCGCGACTCTACTATTTCAAAA 1178
Qy 93 lIePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGln 112
Db 1179 AAATGGGCAAGTACAGCTATTTTAAAGGAAATTTCTTACTTGCATGGGCTCAAG 1238
Qy 1133 LeuValSerGlnLeuThrThrLysGluProLeuTyrHisAsnLeuIleThrIlePheAsn 132
Db 1239 CATTATCTGAATCAGT-----GATACTCGTGCCATTCGACCATTT-----TCT 1283
Qy 1333 GluGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeu 152
Db 1284 AAATCAATTTGTTGATGTGTGTAGAGAGAACTATTTC-----CAATTTCAA 1328
Qy 1533 ProGluIleIleProThrGlnGluMet-----TyrLeuAsnMetValMetAsnLysThr 170
Db 1329 GATCAATTTAATAGCAATCAACAATTAATACTTACTTACGTCGTATCAACCGTAACAA 1388
Qy 171 GlyGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerSerHisHis 190
Db 1389 GCACCTCTTATTCAACTGTCTACACAAGTTGGTGGGATTACTTCCAATTCGTCACAAATGAC 1448
Qy 191 -----GlyHisSerLeuValProPheIleAsnLeuGly 202
Db 1449 GTTATTCGTAAATTAATAATGATCGGACAT-----TATATAGGT 1487
Qy 203 lIeIleTyrGlnIleArgAspTyrLeuAsnLeuLysAspPheGlnMetSerSerGlu 222
Db 1488 ATGAGTTTCCAAATTAATAGATGATGCTGTAGATTTTACTAGTTCTGAAAGAACTTGGT 1547
Qy 223 LysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHisAlaLeu 242
Db 1548 AAGCGGTTGGTAGTCACCTTATGAATGCTCATATTACATTACCTTGCTACTATTAGAAATG 1607
Qy 243 AsnPheThrLysThr-----LysGlyGlnThrGluGlnHis 254
Db 1608 CGAAAAAATATAGACTTTTAAAGATAAAAATTTCAACAATTAATCTCGACAGCTCTCAACAT 1667
Qy 255 AsnGluIleLeuArgIleLeuLeuArgThrSerAspLysAspIleLysLeuLysLeu 274
Db 1668 GCCTTTGAAACTTGTTAATACATATATTAGACAGTCGGAAGCATAGAACATCAAAACAA 1727
Qy 275 lIeGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGln 294
Db 1728 ATA-----AGTGAAAAAGTATTTAAATAAA 1751
Qy 295 LeuValAsnMetIleLys-----AsnAspAsnGluAsnLysTyrLeu 308
Db 1752 GCAATCAATTTAATCGATGAATTAGAGGATGGTCTTAATAAAGAACTA 1799
```

RESULT 11

```
US-11-098-686-9307
; Sequence 9307, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9307
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
; US-11-098-686-9307
```

```
Alignment Scores:
Pred. No.: 4,65e-08 Length: 903
Score: 164.50 Matches: 66
Percent Similarity: 40.0% Conservative: 52
Best Local Similarity: 22.4% Mismatches: 126
Query Match: 9.6% Indels: 51
DB: 12 Gaps: 8

US-10-041-018-22 (1-335) x US-11-098-686-9307 (1-903)

Qy 21 SerLeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeu 40
Db 100 TCTACCCCTTCAACAGCGCTATGAACCTATAGTTTACTTTCGAGGAGGAAAAAGACTAAGAGCT 159
Qy 41 AsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleVal 60
Db 160 GTATTATGTATTTCTTCAGCAGCAGCTTTTGTGCTTAGCCCTACCTCTATTATTTACCTTTT 219
Qy 61 SerGlnIleValGluLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGlu----- 78
Db 220 GCTGCTGGCAATGAAATGATACATCTACTCTACTCAATTAATTCATGACGATTTGCTTGAATG 279
Qy 79 AspAsnAlaProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSer 98
Db 280 GATGATGATGATTTTCGTAGAGGTAAAGCCTTCTGTCTATAAAGCCCTTTAATGAAGCTTTTA 339
Qy 99 ThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThr 118
Db 340 GCTATTCTTCGAGGGAGCGCAGCTATTAAACAGATGCTTTTACCTTCATGATGATACATTA--- 396
Qy 119 ThrLysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuLeuLeu 138
Db 397 -----AACTCTATAGTACCATCTCAACAATATATATTAGTTGCAATT 435
Qy 139 His-----ArgGlyGlnGlyLeuAspIle 146
Db 436 CATGAAATAGCTCAACAGAGCTGGAAGTAAAGTAAAGGAGGAGCTGCGATGATATA 495
Qy 147 TyrTrpArgAspPheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetVal 166
Db 496 -----GAGCATACTGGTGTATCCGATGTCGTCTTTTAATACACTA 534
Qy 167 Met-----AsnLysThrGlyLeuPheArgLeuThrLeuArgLeuMetGlu 182
Db 535 TGCATAATACATGAATATAAAACTGGAGCCCTATTTCGTGTCATCATGTACTACAGCGCT 594
Qy 183 AlaLeuSerProSerSerHisGly---HisSerLeuValProPheIleAsnLeu 201
Db 595 ATGTTAGCTGGAGCAAAATGAATCTGCAATTTATGCTTTTAAATGTTTATCGGGAGCACTA 654
Qy 202 GlyIleIleTyrGlnIleArgAspTyrLeuAsnLeuLysAspPheGlnMetSerSer 221
Db 655 GGTGCAGCTTTCCTCAATTAACCTGATATATCTTAATGTTTACTGCAGATAGTATAACCCCTT 714
Qy 222 GluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHisAla 241
Db 715 CGAAAAACCAACTAGAAAGTGCATCAGGAAAAAGGAAAAATAACATATCTCTCCCTA----- 768
Qy 242 LeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArgIleLeu 261
Db 769 CTAGGACTTGAAGAAAGTAAA----- 789
Qy 262 LeuLeuArgThrSerAspLysAspIleLysLeuLysLeuIleGlnIleLeuGluPheAsp 281
Db 790 -----AAATTAGCTGAAGAAAAAATACATCTTGCAATATCTAGCTAGATCTTTTACT 843
Qy 282 ThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeuVal 296
Db 844 GCGCATGAAGTTTATTCTTAAAGAGGTTGCAAAATAGTCTTTTA 888

RESULT 12
US-11-194-246-139
```

[illegible]

[illegible]

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	46.2	2.9	96988	12	US-11-117-187-196	Sequence 196, App
2	44.6	2.8	845	6	US-09-925-065A-748963	Sequence 748963, App
3	44.4	2.8	6583	8	US-10-240-708-25	Sequence 25, Appl
4	44.2	2.8	645	6	US-09-925-065A-748964	Sequence 748964, App
5	43.8	2.8	623	6	US-09-925-065A-292262	Sequence 292262, App
6	42.6	2.7	602	6	US-09-925-065A-203862	Sequence 203862, App
7	42.6	2.7	658	6	US-09-925-065A-913429	Sequence 913429, App
8	42.6	2.7	28536	12	US-11-011-332A-151	Sequence 151, App
9	42.6	2.7	28536	12	US-11-011-332A-155	Sequence 155, App
10	42.4	2.7	642	6	US-09-925-065A-612196	Sequence 612196, App
11	41.8	2.7	2546	8	US-10-750-185-31825	Sequence 11825, A
12	41.8	2.7	2546	8	US-10-750-623-31825	Sequence 31825, A
13	41.6	2.7	200	12	US-11-098-686-2978	Sequence 2978, App
14	41.6	2.7	598	6	US-09-925-065A-323715	Sequence 323715, App
15	41.6	2.7	1457619	12	US-11-098-686-8739	Sequence 8739, App
16	41.4	2.6	600	8	US-10-750-185-469	Sequence 469, App
17	41.4	2.6	600	8	US-10-750-623-469	Sequence 469, App
18	41.2	2.6	5152	8	US-10-240-708-73	Sequence 73, Appl
19	40.8	2.6	543	6	US-09-925-065A-98741	Sequence 98741, A
20	40.8	2.6	543	6	US-09-925-065A-98743	Sequence 98743, A

```

QY 1346 CAGAAATAAGCCTTCTCTCCTC--CTCTTTCATCTATACATACAGATTTTCATATATAC 1403
Db 61250 ATACATATTTAAATTTATTTCTCATTTCTTTGGTTGAATAGATTTAAATAATAAATTTGTG 61309
QY 1404 GTTTCATGTCATCATCTTTTGTATATATCTCAAAAGATCTCTTAGTTCGCAAAATAGTCAA 1463
Db 61310 GTTTATTTATGTCATCTTTTAAATTTCTCAATATATTTTGGTGTCTATTTATGCTCTA 61369
QY 1464 ATCTTCAAAATTTATAGCCTTTATAT 1488
Db 61370 AAAAACTTTGTAATGCTATTTTGT 61394

```

RESULT 2

US-09-925-065A-748963/c
; Sequence 748963, Application US/09925065A
; Publication No. US20040181048A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 748963

; LENGTH: 645

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-748963

Query Match 2.8%; Score 44.6; DB 6; Length 645;
Best Local Similarity 47.6%; Pred. No. 5;
Matches 131; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

```

QY 181 GAGCTTTTTCGAGCAAAAGAAAGCTCAAGACAGATGTCTTACAAAACCATGTAAGGC 240
Db 550 GAACATTTTTCACAAAACATATCTTTATATAAATCAACTCAAGATAGTTAATAAAGC 491
QY 241 TCATTTTCAAGAGCTACTAATAGAAAGAGACAAAGAGTTTACGAGTCTCGAAATCA 300
Db 490 TGATAGATATTAAATGTATAAAGAAAGCAATGAATAAGCAACTAGAAATATTAGAAAAACA 431
QY 301 ATGGAGGCCAAGATAGATAGCTAGTCAATATATGATCCTGTGTCAGCCAAATGAA 360
Db 430 ATAGAAAATAAAGTAACTAGTGTCACTAAAACCTGATCCTATATAAAGTCACCCAAATGCT 371
QY 361 AGCTTGATTTCAAAACCTTATATACATCCTTTTGAACCTGGCAAGAACTTTAGACTA 420
Db 370 GGGCTCGGTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAAGTA 311
QY 421 AATTTAATAGTTCAATTAACAGAGTTATGAATTT 455
Db 310 AATACATCTTCTTAATTTATATATATATATATATATATATATATATATATATATATAT 276

```

RESULT 3

US-10-240-708-25/c

; Sequence 25, Application US/10240708

; Publication No. US20050282157A1

; GENERAL INFORMATION:

; APPLICANT: OLEK, Alexander

```

; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019059.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 25
; LENGTH: 6583
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-25

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Query Match 2.8%; Score 44.4; DB 8; Length 6583;
Best Local Similarity 51.0%; Pred. No. 12;
Matches 105; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

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QY 1022 CCCTTAACCTTCACTAAACGAAAGGTCAAACTGAGCAACACAAATGCTTAAGAAATTC 1081
Db 5235 CCTCAAAACCAAAATTTCAAAAAAACAATCTCTTACCTCTCAAAATATATATCTAAAAAAT 5176
QY 1082 TCCTGTTGAGGACAAGTGATAAAGATATAAACTAAAGCTGATTCAAATCTGGAATTCG 1141
Db 5175 TTTCTCTACTCCGAAAAAAGCAATATATATATATATATATATATATATATATATATAT 5116
QY 1142 ACACCAATTCATTTGGCCTACACCAAAATTTTATTAATCAATAGTGAATATGATAAAA 1201
Db 5115 AAACCAAAACAAATATCTCGAATATATTTCTTCTTTAACGTAATAAAAAATAACTAAAT 5056
QY 1202 ATGATAATGAAATAAGTATTTACCT 1227
Db 5055 ACGATAATAAAAAATAACTATATACAT 5030

```

RESULT 4

US-09-925-065A-748964/c
; Sequence 748964, Application US/09925065A
; Publication No. US20040181048A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 748964

; LENGTH: 645

; TYPE: DNA

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; ORGANISM: Homo sapiens
US-09-925-065A-748964

Query Match      2.8%; Score 44.2; DB 6; Length 645;
Best Local Similarity 47.3%; Pred. No. 6.1;
Matches 130; Conservative 1; Mismatches 144; Indels 0; Gaps 0;

Qy 181 GACCTTTTGAAGCAAAAGGCTCAAGACAGATGCTTACAAAGCAATGTAAGGC 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
550 GAACATTTTACAAAACATATCTTTTATAAACTAACTCCAGAGATAGTTAATAAGC 491
Qy 241 TCATTTTCAAGAGCTACTAATAGAAAGAGAAACAAAGAGTTTACGAGTCTGGAATCA 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
490 TGATAGAATATTAAATGTAAGAAAGAACATGAATAAAGCAACTAGAAATATTAGAAACA 431
Qy 301 ATGGAGCCCAAGATAGATGCTGATCAATTAATGATCTCTGTTGGTCCAGCCAAATGAA 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
430 ATAGAAATAAAGTAAGTGAAGTTCACATAAAAGTATCTATATAAAGTCAACCCAAATGCT 371
Qy 361 AGCTTGATTTCAAAACCTTATAATCACATCCTTTTGAACCTGGCAAGAACTTTAGACTA 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
370 GGGCTCTGGGTATATATTAATAAATAAATAAATAAATAAATAAATAAATAAAGTA 311
Qy 421 AATTTAATAGTTCAAATTAACAGAGTTTATGAATTT 455
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
310 AATACATCTCTTCTTAATTTATACCTAAAGAAATTT 276

RESULT 5
US-09-925-065A-292262
; Sequence 292262, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292262
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-292262

Query Match      2.8%; Score 43.8; DB 6; Length 623;
Best Local Similarity 54.0%; Pred. No. 7.4;
Matches 87; Conservative 1; Mismatches 73; Indels 0; Gaps 0;

Qy 1070 TTCTAGAATTCCTCTGCTGGAGCAAGTATGAAGATATAAAGCTAAAGCTGATTCAAA 1129
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
263 TTCTCCGATTTGTTATGTTGGTGGCAATTCACAAAATATATACCTCTAAAGACTCATCGAA 322
Qy 1130 TACTGGAATTCGACCAACCAATTCATTTGGCTCACACAAAATTTTATTAACTCAATAGTGA 1189
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
323 TATGGGCAATTTACTGCATTAATTAATGATCGATTAATAATTTATCTTTAAATAAATGA 382
Qy 1190 ATATGATAAAAAATGATAAATGAATAAATGAAATGATTTTACCTGAT 1230
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
383 ACAAGCCAGGATAAAACCAAGATAAATAGTAGTACTTACCTCAT 423

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RESULT 6
US-09-925-065A-203862/c
; Sequence 203862, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203862
; LENGTH: 602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-203862

Query Match      2.7%; Score 42.6; DB 6; Length 602;
Best Local Similarity 48.9%; Pred. No. 13;
Matches 114; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

Qy 1260 TTTCATGACGAATGTTATATATATATATATATATATATATATATATATATATATATAT 1319
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
588 TTAATACTACAAATGCTTGAATTTTGAACCTCTTGAATATGCAATTTTAAATTTGCT 529
Qy 1320 CAATCAAAATAGTGGAGGAGATAGTCAGAAATATAGCCCTTCTCTCTCTCTCTCTCTCCAT 1379
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
528 CTTTCAATTTGCTGGTGTAGTATACAGAAAACAGTTGACATTTTGTATTTTGACCTC 469
Qy 1380 CTATACATACGATTTTCATATATATATATATATATATATATATATATATATATATATAT 1439
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
468 ATATCTTACCTTGTCTAAATTTATTTATTTAGTTCTAGAGTTTCTTAGATTTCTTTTG 409
Qy 1440 ATCTCTTAGTCCAAATAGTCAAAATCTTCAAAATTTATAGCCTTTATATTTT 1492
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
408 ATTTTTCACACTGATAATTTAATTTGCAAAATAAATATATATATATATATATTTCT 356

RESULT 7
US-09-925-065A-913429
; Sequence 913429, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086

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OM nucleic - nucleic search, using sw model

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(without alignments)
9587.015 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1008	64.2	1008	6	US-10-369-493-46181
3	1008	64.2	1008	7	US-10-450-941-5
4	568.6	36.2	1599	9	US-10-487-901-363
5	114	7.3	1395	6	US-10-189-268-4
6	114	7.3	1692	3	US-09-814-353-21762
7	114	7.3	2534	7	US-10-041-018-3
8	113.6	7.2	2529	3	US-09-925-302-171
9	113.6	7.2	2529	3	US-09-925-302-171
10	102.6	6.5	1044	6	US-10-369-493-36092
11	99.6	6.3	1888	8	US-10-357-930-25125
12	90.6	5.8	1284	6	US-10-369-493-27908
13	87.5	5.6	51001	6	US-10-189-268-11
14	84.2	5.4	2210	10	US-11-097-143-9632
15	84.2	5.4	2222	7	US-10-041-018-21
16	70.6	4.5	1882	7	US-10-001-192A-14
17	68.8	4.4	554	3	US-09-969-034-1324
18	68.4	4.4	716	3	US-09-969-034-1924
19	65.6	4.2	593	3	US-09-969-034-1488
20	62.4	4.0	1843	7	US-10-041-018-5
21	60	3.8	399	8	US-10-357-930-49920
22	58.6	3.7	1095	7	US-10-282-122A-40388
23	58.6	3.7	1364	6	US-10-369-493-36669

ALIGNMENTS

RESULT 1

US-10-041-018-1
; Sequence 1, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041, 018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-041-018-1

Query Match	100.0%	Score 1569;	DB 7;	Length 1569;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1569;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	AATATTACATATAGATAGGCAAGCCGCATTTTCATCTACTGAAAGGTAACCTTCTATT	60	
Db	1	AATATTACATATAGATAGGCAAGCCGCATTTTCATCTACTGAAAGGTAACCTTCTATT	60	
Qy	61	ATTATAGTGTATCCAAAGTTTCCAGCTTCCAGCATAGAGAAATAGCGTTTTCGCAT	120	
Db	61	ATTATAGTGTATCCAAAGTTTCCAGCTTCCAGCATAGAGAAATAGCGTTTTCGCAT	120	
Qy	121	ATGTTATGCTGATCATTTGATGCTTACTACCAATTTTCTTTGCTTCGCTTTCCTTT	180	
Db	121	ATGTTATGCTGATCATTTGATGCTTACTACCAATTTTCTTTGCTTCGCTTTCCTTT	180	
Qy	181	GAGCTTTTGTGAAGCAAAAAGTCAAGACAGATGCTTACAAAACCATGTAAGGC	240	
Db	181	GAGCTTTTGTGAAGCAAAAAGTCAAGACAGATGCTTACAAAACCATGTAAGGC	240	
Qy	241	TCATTTTCAAGAGAGTACTTAATAGAAAGACAAAGAGTTTACGAGTCTGGAATCA	300	
Db	241	TCATTTTCAAGAGAGTACTTAATAGAAAGAGTCTTAATAGAAAGAGTTTACGAGTCTGGAATCA	300	
Qy	301	ATGAGGCCAAGATAGATGAGCTGATCAATATGATCTCTGTTGGTCCAGCCAAATGAA	360	

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Db 301 ATGGAGCCCAAGATAGATGAGCTGATCAATAATGATCCTGTGTGGTCCAGCCAAATGAA 1440
QY 361 AGCTTGATTTCAAAACCTTATATACATCCTTTTGAACCTGGCAAGAACTTTAGACTA 1500
Db 361 AGCTTGATTTCAAAACCTTATATACATCCTTTTGAACCTGGCAAGAACTTTAGACTA 1500
QY 421 AATTTAATAGTTCAAAATTAACAGAGTTATGAATTTGGCCCAAGACAGCTGGCCATAGTT 1560
Db 421 AATTTAATAGTTCAAAATTAACAGAGTTATGAATTTGGCCCAAGACAGCTGGCCATAGTT 1560
QY 481 TCGCAAAATTTGAGCTCTTGCATATATCCAGCTTTTAAATCGACATATAGAGTAAT 540
Db 481 TCGCAAAATTTGAGCTCTTGCATATATCCAGCTTTTAAATCGACATATAGAGTAAT 540
QY 541 GCTCCCTTCAGAGGGGACAGACCACTTCTCACTAAATCTTCGGTGTACCTCCACTATA 600
Db 541 GCTCCCTTCAGAGGGGACAGACCACTTCTCACTAAATCTTCGGTGTACCTCCACTATA 600
QY 601 AACACCGCAAAATTAATGATTTTTCAGAGCCATGCAACTTGTATCGCAGCTAAACCAAAA 660
Db 601 AACACCGCAAAATTAATGATTTTTCAGAGCCATGCAACTTGTATCGCAGCTAAACCAAAA 660
QY 661 GAGCCTTTCTATCAATAATTTGATTAGATTTTCAACGAGAAATGATCAATCTACATAGG 720
Db 661 GAGCCTTTCTATCAATAATTTGATTAGATTTTCAACGAGAAATGATCAATCTACATAGG 720
QY 721 GGCAAGGCTTGGATATATACCTGGAGAGACTTCTGCCTGAAATCATACCTACTCAGAGAG 780
Db 721 GGCAAGGCTTGGATATATACCTGGAGAGACTTCTGCCTGAAATCATACCTACTCAGAGAG 780
QY 781 ATGATTTTGAATAATGTTTATGAATAAAGAGGCGCTTTTTCAGATTAACGTTGAGACTC 840
Db 781 ATGATTTTGAATAATGTTTATGAATAAAGAGGCGCTTTTTCAGATTAACGTTGAGACTC 840
QY 841 ATGGAGCCCTGCTCTCTCTCCACACAGGCGCATTCGTTGGTTCCTTTTCATAATCTT 900
Db 841 ATGGAGCCCTGCTCTCTCTCCACACAGGCGCATTCGTTGGTTCCTTTTCATAATCTT 900
QY 901 CTGGGTATTTATTTATCAGATTAGAGATGATTCTGAAATTTGAAAGATTTCCAAATGTCC 960
Db 901 CTGGGTATTTATTTATCAGATTAGAGATGATTCTGAAATTTGAAAGATTTCCAAATGTCC 960
QY 961 AGCGAAAAAGGCTTTGCTGAGGACATTAAGAGGGGAAATTAATTTTCCCATGTCAC 1020
Db 961 AGCGAAAAAGGCTTTGCTGAGGACATTAAGAGGGGAAATTAATTTTCCCATGTCAC 1020
QY 1021 GCGCTTTAACTTCACTAAAGCAAGGTCAACCTGAGCAACACAAATGATTAAGAAAT 1080
Db 1021 GCGCTTTAACTTCACTAAAGCAAGGTCAACCTGAGCAACACAAATGATTAAGAAAT 1080
QY 1081 CTCCTGTCAGGACAAATGATTAAGATATAAAGCTGATTAAGCTGATTAAGCTGATTAAG 1140
Db 1081 CTCCTGTCAGGACAAATGATTAAGATATAAAGCTGATTAAGCTGATTAAGCTGATTAAG 1140
QY 1141 GACACCAATTCATTTGCGCTTACCAAAAATTTTATTAATCAATAGTGAATATGATAAAA 1200
Db 1141 GACACCAATTCATTTGCGCTTACCAAAAATTTTATTAATCAATAGTGAATATGATAAAA 1200
QY 1201 AATGATAATGAATAATGATTAATTTACCTGATTTGGCTTCGCAATTCGACACCCCAAT 1260
Db 1201 AATGATAATGAATAATGATTAATTTACCTGATTTGGCTTCGCAATTCGACACCCCAAT 1260
QY 1261 TTACATGACGAATTTGTTATATATATAGACCACTTATCGAAATGGAATTAATTTGATC 1320
Db 1261 TTACATGACGAATTTGTTATATATATAGACCACTTATCGAAATGGAATTAATTTGATC 1320
QY 1321 AATCAAAATTTAGTGAGGAAGATAGTCAGAAATAAAGCCCTTCTCTCTCTTTTCCGATC 1380
Db 1321 AATCAAAATTTAGTGAGGAAGATAGTCAGAAATAAAGCCCTTCTCTCTCTTTTCCGATC 1380
QY 1381 TATACATAGATTTTCAATATAGCTTTTCAATGATCATCTTTTGAATATATCTCAAAAAGA 1440

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Db 1381 TATACATAGATTTTCAATATAGCTTTTCAATGATCATCTTTTGAATATCTCAAAAAGA 1440
QY 1441 TCTCTTAGTTCCAAATAGTCAAAATCTTCAAAATTTATAGCCTTTATATTTTCCACGAT 1500
Db 1441 TCTCTTAGTTCCAAATAGTCAAAATCTTCAAAATTTATAGCCTTTATATTTTCCACGAT 1500
QY 1501 TTCTGAACCTCTTTTATATAGCAGCAGCTTAAATGCTAGCGGTTACTGCTCAAAATCGCCGTA 1560
Db 1501 TTCTGAACCTCTTTTATATAGCAGCAGCTTAAATGCTAGCGGTTACTGCTCAAAATCGCCGTA 1560
QY 1561 AATTTCGCGA 1569
Db 1561 AATTTCGCGA 1569

RESULT 2
US-10-369-493-46181
; Sequence 46181, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 46181
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-46181

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Query Match 64.2%; Score 1008; DB 6; Length 1008;
Best Local Similarity 100.0%; Pred. No. 1.5e-229;
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 ATGGAGCCCAAGATAGATGAGCTGATCAATAATGATCCTGTGTGGTCCAGCCAAATGAA 360
Db 1 ATGGAGCCCAAGATAGATGAGCTGATCAATAATGATCCTGTGTGGTCCAGCCAAATGAA 60
QY 361 AGCTTGATTTCAAAACCTTATATACATCCTTTTGAACCTGGCAAGAACTTTAGACTA 420
Db 61 AGCTTGATTTCAAAACCTTATATACATCCTTTTGAACCTGGCAAGAACTTTAGACTA 120
QY 421 AATTTAATAGTTCAAAATTAACAGAGTTATGAATTTGGCCCAAGACAGCTGGCCATAGTT 480
Db 121 AATTTAATAGTTCAAAATTAACAGAGTTATGAATTTGGCCCAAGACAGCTGGCCATAGTT 180
QY 481 TCGCAAAATTTGAGCTCTTGCATATATCCAGCTTTTAAATCGACATATAGAGTAAT 540
Db 181 TCGCAAAATTTGAGCTCTTGCATATATCCAGCTTTTAAATCGACATATAGAGTAAT 240
QY 541 GCTCCCTTCAGAGGGGACAGACCACTTCTCACTAAATCTTCGGTGTACCTCCACTATA 600
Db 241 GCTCCCTTCAGAGGGGACAGACCACTTCTCACTAAATCTTCGGTGTACCTCCACTATA 300
QY 601 AACACCGCAAAATTAATGATTTTTCAGAGCCATGCAACTTGTATCGCAGCTAAACCAAAA 660
Db 301 AACACCGCAAAATTAATGATTTTTCAGAGCCATGCAACTTGTATCGCAGCTAAACCAAAA 360
QY 661 GAGCCTTTCTATCAATAATTTGATTAGATTTTCAACGAGAAATGATCAATCTACATAGG 720
Db 361 GAGCCTTTCTATCAATAATTTGATTAGATTTTCAACGAGAAATGATCAATCTACATAGG 420
QY 721 GAGCAGGCTTCGATATATATCTGGAGAGACTTTCGCTGAAATCATACCTACTCTCAGGAG 780

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Db 421 GGACAGGCTTGGATATATATCTGAGAGACTTTCTGCTGAAATCATACCTACTCAGGAG 480
 Qy 781 ATGTATTGTAATATGTTATGAATAAACAAGCGGCGCTTTTTCAGATTAAAGTTGAGACTC 840
 Db 481 ATGTATTGTAATATGTTATGAATAAACAAGCGGCGCTTTTTCAGATTAAAGTTGAGACTC 540
 Qy 841 ATGGAAGCGCTGCTCTCTCTCTCTCACACAGCGCAATTCGTTGGTTCCTTTTCATATAATCTT 900
 Db 541 ATGGAAGCGCTGCTCTCTCTCTCTCACACAGCGCAATTCGTTGGTTCCTTTTCATATAATCTT 600
 Qy 901 CTGGGTATTATTATCAGATTAGAGATGATTACTTGAATTTGAAAGATTTTCCAAATGTCC 960
 Db 601 CTGGGTATTATTATCAGATTAGAGATGATTACTTGAATTTGAAAGATTTTCCAAATGTCC 660
 Qy 961 AGCGAAAGCGCTTTCCTGAGGACATTACAGAGGGAAGTTATCTTTTCCCATCGTCCAC 1020
 Db 661 AGCGAAAGCGCTTTCCTGAGGACATTACAGAGGGAAGTTATCTTTTCCCATCGTCCAC 720
 Qy 1021 GCCCTTAACCTTCACTAAAAAGGTCAAACTGAGCAACCAATGAAATTTCTAAGAATT 1080
 Db 721 GCCCTTAACCTTCACTAAAAAGGTCAAACTGAGCAACCAATGAAATTTCTAAGAATT 780
 Qy 1081 CTCCTGTGAGGACAAGTATAAGATATAAATAAAGCTGATTCAAATGAAATTTCTAAGAATT 1140
 Db 781 CTCCTGTGAGGACAAGTATAAGATATAAATAAAGCTGATTCAAATGAAATTTCTAAGAATT 840
 Qy 1141 GACACCAATTCATTTGGCTTACACCAAAAATTTTATTAATCAATTTAGTGAATGATATAA 1200
 Db 841 GACACCAATTCATTTGGCTTACACCAAAAATTTTATTAATCAATTTAGTGAATGATATAA 900
 Qy 1201 AATGATAAGTAAATAGTATTACCTGATTGGCTTCGCAATCCGACACCGCCACCAAT 1260
 Db 901 AATGATAAGTAAATAGTATTACCTGATTGGCTTCGCAATTCGCAATCCGACACCGCCACCAAT 960
 Qy 1261 TTACATGACGAATTTGTTATATATATATAGACCACTTATCCGAATTTGTGA 1308
 Db 961 TTACATGACGAATTTGTTATATATATATAGACCACTTATCCGAATTTGTGA 1008

RESULT 3

US-10-450-941-5
 ; Sequence 5, Application US/10450941
 ; Publication No. US20040063182A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
 ; TITLE OF INVENTION: A METHOD OF PRODUCING PRENYLALCOHOL
 ; FILE REFERENCE: PH-144PCT
 ; CURRENT APPLICATION NUMBER: US/10/450,941
 ; CURRENT FILING DATE: 2003-06-18
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: JP2000-401701
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: JP2000-403067
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: JP2001-282978
 ; PRIOR FILING DATE: 2001-09-18
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 1008
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces cerevisiae
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1005)
 US-10-450-941-5

Query Match 64.2%; Score 1008; DB 7; Length 1008;
 Best Local Similarity 100.0%; Pred. No. 1.5e-229; Indels 0; Gaps 0;
 Matches 1008; Conservative 0; Mismatches 0;
 Qy 301 ATGAGGCCAAGATAGATGAGCTGATCAATAATGATCCTGTTGGTCCAGCCAAATGAA 360
 Db 1 ATGAGGCCAAGATAGATGAGCTGATCAATAATGATCCTGTTGGTCCAGCCAAATGAA 60

Qy 361 AGCTTGATTTCAAAACCTTATAATCACATCCTTTTGAACCTGGCAAGAACCTTTAGACTA 420
 Db 61 AGCTTGATTTCAAAACCTTATAATCACATCCTTTTGAACCTGGCAAGAACCTTTAGACTA 120
 Qy 421 AATTTAATAGTTCAAAATTAACAGAGTTATGAAATTTGCCAAAGACAGCTGGCCATAGTT 480
 Db 121 AATTTAATAGTTCAAAATTAACAGAGTTATGAAATTTGCCAAAGACAGCTGGCCATAGTT 180
 Qy 481 TCCCAATTCCTGAGCTCTTGCATATTCAGAGCTTTTAATCGACGATATAGAGATAAT 540
 Db 181 TCCCAATTCCTGAGCTCTTGCATATTCAGAGCTTTTAATCGACGATATAGAGATAAT 240
 Qy 541 GCTCCCTTGAAGAGGAGACAGACCTTCTCACTTAATCTTGGTGATACCTCCACTATA 600
 Db 241 GCTCCCTTGAAGAGGAGACAGACCTTCTCACTTAATCTTGGTGATACCTCCACTATA 300
 Qy 601 AACACCGCAAAATTAATATGTAATTTTCAGAGCCATGCAACTTGTATCGCAGCTAACCAAAA 660
 Db 301 AACACCGCAAAATTAATATGTAATTTTCAGAGCCATGCAACTTGTATCGCAGCTAACCAAAA 360
 Qy 661 GAGCCTTTGTATCATTAATTTGATTCAGATTTTCAACGAAGAAATTTGATCAATCTACATAGG 720
 Db 361 GAGCCTTTGTATCATTAATTTGATTCAGATTTTCAACGAAGAAATTTGATCAATCTACATAGG 420
 Qy 721 GGACAAAGGCTTGGATATATCTGAGAGACTTTCTGCTCGAAATCATACCTACTCAGGAG 780
 Db 421 GGACAAAGGCTTGGATATATCTGAGAGACTTTCTGCTCGAAATCATACCTACTCAGGAG 480
 Qy 781 ATGTATTGTAATATGTTATGAATAAACAAGCGGCGCTTTTTCAGATTAAAGTTGAGACTC 840
 Db 481 ATGTATTGTAATATGTTATGAATAAACAAGCGGCGCTTTTTCAGATTAAAGTTGAGACTC 540
 Qy 841 ATGGAAGCGCTGCTCTCTCTCTCACACAGCGCAATTCGTTGGTTCCTTTTCATATAATCTT 900
 Db 541 ATGGAAGCGCTGCTCTCTCTCTCACACAGCGCAATTCGTTGGTTCCTTTTCATATAATCTT 600
 Qy 901 CTGGGTATTATTATCAGATTAGAGATGATTACTTGAATTTGAAAGATTTTCCAAATGTCC 960
 Db 601 CTGGGTATTATTATCAGATTAGAGATGATTACTTGAATTTGAAAGATTTTCCAAATGTCC 660
 Qy 961 AGCGAAAGCGCTTTCCTGAGGACATTACAGAGGGAAGTTATCTTTTCCCATCGTCCAC 1020
 Db 661 AGCGAAAGCGCTTTCCTGAGGACATTACAGAGGGAAGTTATCTTTTCCCATCGTCCAC 720
 Qy 1021 GCCCTTAACCTTCACTAAAAAGGTCAAACTGAGCAACCAATGAAATTTCTAAGAATT 1080
 Db 721 GCCCTTAACCTTCACTAAAAAGGTCAAACTGAGCAACCAATGAAATTTCTAAGAATT 780
 Qy 1081 CTCCTGTGAGGACAAGTATAAGATATAAATAAAGCTGATTCAAATGAAATTTCTAAGAATT 1140
 Db 781 CTCCTGTGAGGACAAGTATAAGATATAAATAAAGCTGATTCAAATGAAATTTCTAAGAATT 840
 Qy 1141 GACACCAATTCATTTGGCTTACACCAAAAATTTTATTAATCAATTTAGTGAATGATATAA 1200
 Db 841 GACACCAATTCATTTGGCTTACACCAAAAATTTTATTAATCAATTTAGTGAATGATATAA 900
 Qy 1201 AATGATAAGTAAATAGTATTACCTGATTGGCTTCGCAATCCGACACCGCCACCAAT 1260
 Db 901 AATGATAAGTAAATAGTATTACCTGATTGGCTTCGCAATTCGCAATCCGACACCGCCACCAAT 960
 Qy 1261 TTACATGACGAATTTGTTATATATATAGACCACTTATCCGAATTTGTGA 1308
 Db 961 TTACATGACGAATTTGTTATATATATAGACCACTTATCCGAATTTGTGA 1008

RESULT 4

US-10-487-901-363
 ; Sequence 363, Application US/10487901
 ; Publication No. US20050091708A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oreido, Jeremiah Vincent
 ; APPLICANT: McCrery, David

```

; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 363
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; US-10-487-901-363

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Query Match	36.2%	Score 568.6;	DB 9;	Length 599;
Best Local Similarity	98.5%;	Pred. No. 6e-125;		
Matches 574;	Conservative	0;	Mismatches 9;	Indels 0;
Gaps	0;			

299	QY	CAATGGAGGCCAAGATAGATGAGCTGATCAATTAATGATCTGTTGGTTCAGGCCAAAATG	358
17	DB	CCATGGAGGCCAACATACATGAGCTGATCAATTAATGATCTGTTGGTTCAGGCCAAAATG	76
359	QY	AAAGCTTGATTTCAAAACCTTTATAATCACATCTCTTTTGAACCTGGCAAGAACTTTAGAC	418
77	DB	AAAGCTTGATTTCAAAACCTTTATAATCACATCTCTTTTGAACCTGGCAAGAACTTTAGAC	136
419	QY	TAAATTTAAATAGTTCAAATTAACAGAGTTATGAATTTGCCCAAAGACCAGCTGGCCATAG	478
137	DB	TAAATTTAAATAGTTCAAATTTAAACAGAGTTATGAATTTGCCCAAAGACCAGCTGGCCATAG	196
479	QY	TTTTCGCAAAATGTTGAGCTCTTGCGATTAATTTCCAGCGCTTTTAAATCGACGATATAGAAGATA	538
197	DB	TTTTCGCAAAATGTTGAGCTCTTGCGATTAATTTCCAGCGCTTTTAAATCGACGATATAGAAGATA	256
539	QY	ATGCTCCCTTGGAGAAGGGGACAGACCACCTCTCACTTTAACTCTCGGTGTACCCCTCCAATA	598
257	DB	ATGCTCCCTTGGAGAAGGGGACAGACCACCTCTCACTTTAACTCTCGGTGTACCCCTCCAATA	316
599	QY	TAAACACCGCAAAATTATATGTATTTACAGGCCATGCAACTTTGTATCGCAGCTAACCCAA	658
317	DB	TAAACACCGCAAAATTATATGTATTTACAGGCCATGCAACTTTGTATCGCAGCTAACCCAA	376
659	QY	AAGAGCCTTTGTATCATATAATTTGATACGATTTTCAACGAAGAATTTGATCAATCTACATA	718
377	DB	AAGAGCCTTTGTATCATATAATTTGATACGATTTTCAACGAAAAATTTGATCAATCTACATA	436
719	QY	GGGGACAAGCCTTGGATATATACCTGGAGAGACCTTTCTGCGCTGGAATCATACCTACTCAGG	778
437	DB	GGGGACAAGCCTTGGATATATACCTGGAGAGACCTTTCTGCGCTGGAATCATACCTACTCAGG	496
779	QY	AGATGTATTTTGAATATCGGTTATGAATAAAAACAGCGCGCCTTTTTCAGATTTAACGTTTGAGAC	838
497	DB	AGATGTATTTTGAATATCGGTTATGAATAAAAACAGCGCGCCTTTTTCAGATTTAACGTTTGAGAC	556
839	QY	TCATGGAAGCGCTGTCTCTCTCCCTCACACCAACGCGCCATTCGTT	881
557	DB	TCATGGAACACGTCTCTCTCTCTCTCACACCAACGCGGCATTCGTT	599

RESULT 5
US-10-189-268-4
; Sequence 4, Application US/10189268
; Publication No. US20040005570A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: C. Frank Bennett

```

; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF GERANYLGERANYL DIPHOSPHATE SYNTH
; FILE REFERENCE: PTS-0021
; CURRENT APPLICATION NUMBER: US/10/189,268
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 4
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)..(1072)
US-10-189-268-4

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Query Match	7.3%;	Score 114;	DB 6;	Length 1395;
Best Local Similarity	52.1%;	Pred. No. 2e-16;		
Matches 348;	Conservative 0;	Mismatches 290;	Indels 30;	Gaps 3;

QY	359	AAAGCTTGATTTCAAAACCTTATAATACATCCTTTTGAACCTGCGCAAGAACTTTAGAC	418
DB	195	AAAGAAATCTCTTAGAACCTATAAATCTTACTTCGATTACAGGTAAACAAAGTGAGAA	254
QY	419	TAAATTTAATAGTTCAAAATTAACAGAGTTTATGAATTTGCCAAAGACCAAGCTGGCCATAG	478
DB	255	CCAAACTTTTACAGGCAATTTAATCATTTGGCTGAAAGTTCCAGAGGACAAGCTACAGATTA	314
QY	479	TTTTCGAAATGTTGAGCTCTTGCGATAATTCAGCGCTTTTAAATCGACGATATAGAAGATA	538
DB	315	TTATTGAAGTGACAGAAATGTTGCGATAATGCCAGTTTACTCATCGATGATATTGAAGACA	374
QY	539	ATGCTCCCTTGAAGGGGACAGACCACTTCTCACTTAATCTTCGGTGACCCCTCCACATA	598
DB	375	ACTCAAAATTCGACGTGGCTTTCCAGTGGCCACAGCATCTATGGAAATCCCATCTGTCTCA	434
QY	599	TAAACACCCGCAAAATTATATGTATTTCCAGAGCCATGCAACTTTGTATCGCAGCTAACACAA	658
DB	435	TCBAATCTCGCAATTTACGTGTATTTCTTTGGCTTGGAGAAAGTCT-----	479
QY	659	AAGAGCCTTTGTATCATAAATTTGATTTACAGATTTTCAACGAAGAAATGTATCAATCTACATA	718
DB	480	TAAACCTTGTATCACCAGATGCGATGGAAGCTTTTACCAGCCAGGCTTTTGGAACTCCATC	539
QY	719	GGGCGACAAGCGCTTGGATATATACTCGAGAGACTTTTCTGCCTGAAATCATACCTTACTCAGG	778
DB	540	AGGGACAGAGCCTAGATATTTACTGGAGGA-----TAAATTACATTTGTCACCTGAAG	593
QY	779	AGATGTATTTGAATATGGTTATGAATATAAACAGCGCGCCTTTTCAGATTAACGTTGAGAC	838
DB	594	AAGAATATAAAGCTATGTTGCTGCAGAAACAGGTGGAAGCTGTTTGGATTAGCAGTAGGTCT	653
QY	839	TGATGAAGCGGTGCTCTCCTCTGTCACACAGCGGCAATCGTTGGTTCTTTTCATATAATC	898
DB	654	TGATGCAAGTTGTTCTCTGATTTCAAGAAGATTTTAAACCGCTACTTT-----AATA	704
QY	899	TTCTCGGTATATTTATCAGATTAGAGATGATTACTTTGAATTTGAAGATTTTCCAAATGT	958
DB	705	CACCTTGGGCTCTTTTCCAAATTAGGGATGATTATGCTAATCTACACTCAAAGAATATA	764
QY	959	CCAGCGAAAAAGGCTTTGCTGAGGACATTTACAGAGGGGAAGTTATCTTTTCCCATCGTCC	1018
DB	765	GTGAAACAAAGATTTTGTGGAAGATCTGACAGAGGGAAGTTCTCATTTCTCTACTATTTC	824
QY	1019	AGCCCTTT	1026
DB	825	ATGCTATT	832

RESULT 6
US-09-814-353-21762
; Sequence 21762, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:

; APPLICANT: Lee, John
 ; APPLICANT: Thompson, Pamela
 ; APPLICANT: Lillie, James
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
 ; FILE REFERENCES: MRI-006B
 ; CURRENT APPLICATION NUMBER: US/09/814,353
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: US 60/191,031
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/207,124
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: US 60/211,940
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: US 60/216,820
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: US 60/220,661
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: US 60/257,672
 ; PRIOR FILING DATE: 2000-12-21
 ; NUMBER OF SEQ ID NOS: 22037
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 21762
 ; LENGTH: 1692
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1, 1692
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-814-353-21762

Query Match 7.3%; Score 114; DB 3; Length 1692;
 Best Local Similarity 52.1%; Pred. No. 2.2e-16;
 Matches 348; Conservative 0; Mismatches 290; Indels 30; Gaps 3;
 359 AAAGCTTGATTTCAAAACCTTATAATCACATCTTTTGAACCTGGCAAGACTTTAGAC 418
 280 AAAGAATCTTCTAGAACCTTATAATATCTTCTAGTTACCAAGGTAACAAGTAGAA 339
 419 TAAATTTAATAGTTTCAAAATTAACAGAGTTATGAATTTGCCAAAGACAGCTGCCATAG 478
 340 CCAAACTTTCACAGGCAATTAATCATTTGGCTGAAAGTTCCAGAGGACAAGCTACAGATTA 399
 479 TTTGCGAAATTTGTGAGCTCTTGCAATATTCACGCTTTTAAATCGACGATATGAAGATA 538
 400 TTATTGAAGTGACAGAAATGTTGCATATGCGAGTTTACTCATCGATGATATTGAAGACA 459
 539 ATGCTCCCTTGAGAGGGGACAGACCACTTCTCACTTAATCTTGGGTGACCTCCACTA 598
 460 ACTCAAACTCCGACGTGGCTTTCCAGTGGCCACAGCATCTATGGAATCCCATCTGTCA 519
 599 TAAACACCGCAAAATTAATATGTTTTCAGAGCCATGCAACTTTGTATCGCAGCTAACCAAA 658
 520 TCAATCTGCAATTAAGTGTATTTCTTGGCTTGGAGAAAGTCT----- 564
 659 AAGAGCTTTGTATCAATAATTTGATAGCAATTTTCAACGAAAGTGAATCAATCTACATA 718
 565 TAAACCTTGTATCAACCCAGATGCAAGCTTTTACCCGCGAGCTTTTGGAACTCCATC 624
 719 GGGGACAGGCTTGGATATATCTGAGAGACTTTCGCTCGAATCATACCTACTCAGG 778
 625 AGGACAGGCTTAGATATTTACTTGGAGGA-----TAAATACCTTGTGCCACTGAAG 678
 779 AGATGTTATTTGAATATGTTTATGAATAAAACAGCGCGCTTTTTCAGATTAACGTTGAGAC 838
 679 AAGNATATAAGCTATGCTGCGAAGAAACAGGTGAGCTTTTGGATTAGCAGTAGGTC 738
 839 TCATGGAAGCGCTGTCTCTTCCCTTCACACACCGGCCAATTCGTTGGTTTCCCTTCAATAATC 898
 739 TCATGCAAGTTGTTCTCTCTGATTACAAAGAGATTAAACCGCTACTT-----AATA 789

899 TTCTGGGTATTTATATCATGATTAGATAGATTACTTGAATTTGAAAGATTTCCAAATGT 958
 790 CACTTGGGCTCTTTTCCAAATTTAGGATGATTATGCTATCTACACTCCAAAGATATA 849
 959 CCAGCGAAAAAGCTTTGCTGAGACATTAACAGAGGGAAGTTATCTTTTCCCATCGTCC 1018
 850 GTGAAAAACAAAGTTTTGTGAAGATCTGACAGAGGGGAAAGTTCTCATTTCTACTATT 909
 1019 ACGCCCTT 1026
 910 ATGCTATT 917
 RESULT 7
 US-10-041-018-3
 ; Sequence 3, Application US/10041018
 ; Publication No. US20040072323A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Matsuda, Seiichi P.T.
 ; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
 ; FILE REFERENCE: P02080US1/10025547
 ; CURRENT APPLICATION NUMBER: US/10/041,018
 ; CURRENT FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: US 60/259880
 ; PRIOR FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 2534
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-041-018-3

Query Match 7.3%; Score 114; DB 7; Length 2534;
 Best Local Similarity 52.1%; Pred. No. 2.7e-16;
 Matches 348; Conservative 0; Mismatches 290; Indels 30; Gaps 3;
 359 AAAGCTTGATTTCAAAACCTTATAATCACATCTTTTGAACCTGGCAAGACTTTAGAC 418
 258 AAAGAATCTTCTAGAACCTTATAATATCTTCTAGTTACCAAGGTAACAAGTAGAA 317
 419 TAAATTTAATAGTTTCAAAATTAACAGAGTTATGAATTTGCCAAAGACAGCTGCCATAG 478
 318 CCAAACTTTCACAGGCAATTAATCATTTGGCTGAAAGTTCCAGAGGACAAGCTACAGATTA 377
 479 TTTGCGAAATTTGTGAGCTCTTGCAATATTCACGCTTTTAAATCGACGATATGAAGATA 538
 378 TTATTGAAGTGACAGAAATGTTGCATATGCGAGTTTACTCATCGATGATATTGAAGACA 437
 539 ATGCTCCCTTGAGAGGGGACAGACCACTTCTCACTTAATCTTGGGTGACCTCCACTA 598
 438 ACTCAAACTCCGACGTGGCTTTCCAGTGGCCACAGCATCTATGGAATCCCATCTGTCA 497
 599 TAAACACCGCAAAATTAATATGTTTTCAGAGCCATGCAACTTTGTATCGCAGCTAACCAAA 658
 498 TCAATCTGCAATTAAGTGTATTTCTTGGCTTGGAGAAAGTCT----- 542
 659 AAGAGCTTTGTATCAATAATTTGATAGCAATTTTCAACGAAAGTGAATCAATCTACATA 718
 543 TAAACCTTGTATCAACCCAGATGCAAGCTTTTACCCGCGAGCTTTTGGAACTCCATC 602
 719 GGGGACAGGCTTGGATATATCTGAGAGACTTTCGCTCGAATCATACCTACTCAGG 778
 603 AGGACAGGCTTAGATATTTACTTGGAGGA-----TAAATACCTTGTGCCACTGAAG 656
 779 AGATGTTATTTGAATATGTTTATGAATAAAACAGCGCGCTTTTTCAGATTAACGTTGAGAC 838
 657 AAGNATATAAGCTATGCTGCGAAGAAACAGGTGAGCTTTTGGATTAGCAGTAGGTC 716
 839 TCATGGAAGCGCTGTCTCTTCCCTTCACACACCGGCCAATTCGTTGGTTTCCCTTCAATAATC 898
 717 TCATGCAAGTTGTTCTCTCTGATTACAAAGAGATTAAACCGCTACTT-----AATA 767

QY 899 TTCTGGGTATTATTCAGATTAGAGATGATTACTTGAATTTGAAGATTTCCTCAATGT 958
Db 768 CACTTGGGCTCTTTTCCAAATTAGGGATGATTATGCTAATCTACACTCCAAGAAATATA 827
QY 959 CCAGCGAAAGAGCTTTGCTGAGGACATTACAGAGGGGAAGTTATCTTTTCCCATCGTCC 1018
Db 828 GTGAACAAAGTTTGTGGAAGTCTGACAGAGGGAAGTTCTCATTTCTCTACTATTC 887
QY 1019 ACGCCCTT 1026
Db 888 ATGCTATT 895
RESULT 8
US-09-925-302-171
; Sequence 171, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 171
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-302-171

Query Match 7.2%; Score 113.6; DB 3; Length 2529;
Best Local Similarity 51.9%; Pred. No. 3.4e-16;
Matches 347; Conservative 1; Mismatches 290; Indels 30; Gaps 3;
QY 359 AAAGCTTGATTTCAAACCTTATAATCAATCATCATCTTTTGAAACCTGGCAAGAACTTTAGAC 418
Db 246 AAGAATCTCTTAGAACCTTATAAATCTTACTTACAGTTACAGGTAACAGTGAGAA 305
QY 419 TAAATTAATAGTTCAAATTAACAGAGTTATGAATTTGCCAAAGACAGCTGGCCATAG 478
Db 306 CCAAACTTTACAGGCATTTATCATTTGGCTGAAAGTTCCAGAGGACAAGCTACAGATTA 365
QY 479 TTTCGCAAAATTTGAGCTCTTGCAATATTCAGCCCTTTTAAATCGACGATATAGAGATA 538
Db 366 TTATTGAAGTGACAGAAATGTTGCATAATGCCAGTTTACTCATCGATGATATTGAAGACA 425
QY 539 ATGCTCCCTTGAGAGGGGACAGACCACTTCTCACTTAATCTTCGGTGTACCTCCACTA 598
Db 426 ACTCAAACTCCGAGTGGCTTTCCAGTGGCCCAAGCATCTATGAAATCCCATCTGTCA 485
QY 599 TAAACACCGCAAAATTAATATGATTTTCAGAGCCATGCAACTTGTATCGCAGTAAACCACAA 658
Db 486 TCAATTTCTGCCAATTAACGTGTAATTTTACCCGCCAGCTTTTGGAACTCCATC 590
QY 719 GGGGCAAGGCTTGGATATATCTGGAGAGACTTTCTGCCTGAAATCATACCTACTCAGG 778
Db 591 AGGCAAGGCTTAGATATTACTGGAGGGA-----TAATTACATTTCTCCACTGAAG 644
QY 779 AGATGATTATGAATATGGTTATGAATAAACAAGGGGCGCTTTTCAGATTAAACGTTGAGAC 838
Db 645 AAGAAATATAAAGCTATGGTCTGCAGAAACAGGTGGAAGTGTGTTGATTTAGCAGTAGGTC 704
QY 839 TCATGGAAGCGCTGTCTCTTCTCTCACACCAAGGCCAATTCGTTGGTTCTTTCATAAATC 898

Db 705 TCATCAGCTGTCTCTGATTAACAAGAGATTTAAAACCGCTACTT-----AATA 755
QY 899 TTCTGGGTATTATTCAGATTAGAGATGATTACTTGAATTTGAAGATTTCCTCAATGT 958
Db 756 CACTTGGGCTCTTTTCCAAATTAGGGATGATTATGCTAATCTACACTCCAAGAAATATA 815
QY 959 CCAGCGAAAGAGCTTTGCTGAGGACATTACAGAGGGGAAGTTATCTTTTCCCATCGTCC 1018
Db 816 GTGAACAAAGTTTGTGGAAGTCTGACAGAGGGAAGTTCTCATTTCTCTACTATTC 875
QY 1019 ACGCCCTT 1026
Db 876 ATGCTATT 883
RESULT 9
US-09-925-302-171
; Sequence 171, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 171
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-302-171

Query Match 7.2%; Score 113.6; DB 3; Length 2529;
Best Local Similarity 51.9%; Pred. No. 3.4e-16;
Matches 347; Conservative 1; Mismatches 290; Indels 30; Gaps 3;
QY 359 AAAGCTTGATTTCAAACCTTATAATCAATCATCATCTTTTGAAACCTGGCAAGAACTTTAGAC 418
Db 246 AAGAATCTCTTAGAACCTTATAAATCTTACTTACAGTTACAGGTAACAGTGAGAA 305
QY 419 TAAATTAATAGTTCAAATTAACAGAGTTATGAATTTGCCAAAGACAGCTGGCCATAG 478
Db 306 CCAAACTTTACAGGCATTTATCATTTGGCTGAAAGTTCCAGAGGACAAGCTACAGATTA 365
QY 479 TTTCGCAAAATTTGAGCTCTTGCAATATTCAGCCCTTTTAAATCGACGATATAGAGATA 538
Db 366 TTATTGAAGTGACAGAAATGTTGCATAATGCCAGTTTACTCATCGATGATATTGAAGACA 425
QY 539 ATGCTCCCTTGAGAGGGGACAGACCACTTCTCACTTAATCTTCGGTGTACCTCCACTA 598
Db 426 ACTCAAACTCCGAGTGGCTTTCCAGTGGCCCAAGCATCTATGAAATCCCATCTGTCA 485
QY 599 TAAACACCGCAAAATTAATATGATTTTCAGAGCCATGCAACTTGTATCGCAGTAAACCACAA 658
Db 486 TCAATTTCTGCCAATTAACGTGTAATTTTACCCGCCAGCTTTTGGAACTCCATC 590
QY 719 GGGGCAAGGCTTGGATATATCTGGAGAGACTTTCTGCCTGAAATCATACCTACTCAGG 778
Db 591 AGGCAAGGCTTAGATATTACTGGAGGGA-----TAATTACATTTCTCCACTGAAG 644
QY 779 AGATGATTATGAATATGGTTATGAATAAACAAGGGGCGCTTTTCAGATTAAACGTTGAGAC 838
Db 645 AAGAAATATAAAGCTATGGTCTGCAGAAACAGGTGGAAGTGTGTTGATTTAGCAGTAGGTC 704

QY 839 TCATGGAAGCGCTGCTCTCTCTCTCACACCGCCCACTGTTGGTTCTCTTTCATTAATC 898
 DB 705 TCATGCAAGTGTCTCTGATTACAAAGATTAAACCGCTACTT-----ATA 755
 QY 899 TTCTGGGTATATTTATCAGATAGATGATGATTACTTGAATTTGAAGATTTCCAAATGT 958
 DB 756 CACTTGGGCTCTTTTCCAAATTAGGATGATTATGCTAATCTACACTCCAAAGATATA 815
 QY 959 CCAGCGAAAAGGCTTGTCTGAGACATTACAGAGGGGAAGTTATCTTTCCCATCGTCC 1018
 DB 816 GTGAAACAAAGTTTGTGAGATCTGACAGAGGGAAGTTCTCATTTCTACTATTTC 875
 QY 1019 ACGCCCTT 1026
 DB 876 ATGCTATT 883
 RESULT 10
 ; Sequence 36092, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 36092
 ; LENGTH: 1044
 ; TYPE: DNA
 ; ORGANISM: Aspergillus nidulans
 ; US-10-369-493-36092

Query Match 6.5%; Score 102.6; DB 6; Length 1044;
 Best Local Similarity 49.9%; Pred. No. 9.2e-14;
 Matches 363; Conservative 0; Mismatches 334; Indels 30; Gaps 3;
 QY 300 AATGAGGCCAAGATGATGAGCTGATCAATATATGATCTGTTGGTCCAGCCAAATGA 359
 DB 153 AAATCAGTCAAGTCTCGACGGGCAAAATACAAAGATGGGAAATGGTCCCAAGAGAATGA 212
 QY 360 AAGCTTGATTTCAAACCTTATATACATCTTTTGAACCTGGCAAGAACTTTAGACT 419
 DB 213 GGAGGTGATCATGGTCCGACGATACATGCTGCAACACCCGGGGAAGGACCTGGGACG 272
 QY 420 AAATTTAATGTTCAAATTAACAGATTTGAAATTTGCCCAAGACCAGCTGGCCATAGT 479
 DB 273 GCAGATGATCAAGCTTTTAAAGTATGTTGAAGTGGCATCTGAGAGCTGGCCATCAT 332
 QY 480 TTCCGAAATTTGAGCTTTGCAATATTCACGCTTTTAAATCGACGATATAGAAGATAA 539
 DB 333 CACCAAGTAGTGGCTATGCTCCATACCGCTTCATTATTGATCGACGCGTGAAGACAA 392
 QY 540 TGCTCCCTTGAAAGGGGACAGACCACTTCTCATTATCTTCGGTGTACCTCCACTAT 599
 DB 393 CTCTCTTCTCCGGGAGGAATTCGGTTCGCACATAGCATCTATGGCACCGCGCAGCAT 452
 QY 600 AAACACGCAAAATATATGATTTTACAGAGCCATGCACTTGTATCGCAGCTTAACCAAA 659
 DB 453 CAATTCGGCAAACTAGCTTTACTTCTCGCCCTCCAGGAGGTGCAAAAATCGAAGTCC 512
 QY 660 AGAGCCCTTTGATCATAATTTGATTAAGATTTTCAACGAAGAATTTGATCAATCTACATAG 719
 DB 513 GGCAGCTATCGAC-----ATATACGTTCCAGGAGCTGCTGTAATTTACACAG 557

QY 720 GGCACAAAGGCTTGGATATATCTGGAGAGACTTTTCTCCCTGAAATCATACTACTCAGGA 779
 DB 558 AGGCAAGGATGATGATCTGTTCTGGCGAGACACGCTCATTGT-----CCACCGAGAA 611
 QY 780 GATGATTTTGAATATGTTATGAATAAAACAGCGGCTTTTTCAGATTAACGTTGAGACT 839
 DB 612 TGAATACTTGGAGATGGTGGGCAACAAGACTCGGAGGTTTGTTCGGGCTAGCTGTGAAAT 671
 QY 840 CATGGAGCGCTCTCTCTCTCTCACACCGGCGCATTCGTTGGTTCCTTTCATAAATCT 899
 DB 672 GATGCAAG-----CTGAAAGCAGCACTGGAAGGAGCTGTGTGGCCCTTGTGAATGT 722
 QY 900 TCTGGGTATTATTATCAGATTAGAGATGATTCTTGAATTTTGAAGATTTTCCAAATGTC 959
 DB 723 TTTGGGACTGCTCTTTCAGATATGCGACGATCTCTCAATTTATCCGACGAGGATATAC 782
 QY 960 CACGCAAAAGGCTTTGCTGAGGACATTACAGAGGGGAAGTTATCTTTTCCCATCGTCCA 1019
 DB 783 CCAGAACAAAGGCTCTGTGGAAGACCTCACAGAGGGCAAAATTTTCATTTCCCATTAATCCA 842
 QY 1020 CGCCCTT 1026
 DB 843 CAGCAT 849
 RESULT 11
 ; US-10-357-930-25125
 ; Sequence 25125, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 25125
 ; LENGTH: 1888
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1, 2, 1888
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-10-357-930-25125

Query Match 6.3%; Score 99.6; DB 8; Length 1888;
 Best Local Similarity 51.8%; Pred. No. 6.4e-13;
 Matches 346; Conservative 0; Mismatches 289; Indels 33; Gaps 4;
 QY 359 AAGCTTGATTTCAAACCTTATTAATCAATCTTTTGAACCTGGCAAGAACTTTAGAC 418
 DB 479 AAAGAATTTCTTCTAGAACCTTATAAATCTTCTTCACTTCTAGTTACCAAGGTAAACAAGTGAGAA 538

QY 419 TAAATTTAATAGTTCMAATTAACAGAGTTATGAATTTGGCCAAAGACCAAGTGGCCATAG 478
 Db 539 CCAAACTTTTCAGAGCATTTAATCATTTGGCTGAAAGTTCCAGAGGACAAAGCTACAGATTA 598
 QY 479 TTTTCGCAAAATTTGAGCTTTGCAATAATTCAGGCTTTTAAATCGACGATATAGAGATA 538
 Db 599 TTATTGAAGTGACAGAAATGTGTCATAATGCCAGTTTACTCATCGATGATATGAAGACA 658
 QY 539 ATGCTCCCTTGAGAGGGGACAGACCACTTCTCACTTAATCTCGGTGTACCTCCACTA 598
 Db 659 ACTCAAACTCCGAGCTGGCTTCCAGTGGCCCAACAGCATCTATGGAATCCCATCTGTCA 718
 QY 599 TAAACACCCCAATATATATGTTTTCAGAGCCATGCAACTTGTATCGCAGCTAAACACAA 658
 Db 719 TCAATTTCTGCCAATACGTGTATTTCTTGGCTTGGAGAAAGTCT----- 763
 QY 659 AAGAGCTTTGTATCATATAATTTGATTTACGATTTTCAACGAAGATTTGATCAATCTACATA 718
 Db 764 TAACCTTTGATCACCAGATGAGTGAAGCTTTTACCCGCCAGCTTTTGGAACTCCATC 823
 QY 719 GGGGCAAGCTTTGGATATATATCTGGAGAGACTTTCTGCTGAAATCATACCTACTCAGG 778
 Db 824 AGGCAAGCTCTAGATATTTACTGGAGGA-----TAATTACACTTGTCCCACTGAAG 877
 QY 779 AGATGATTTGAATATGTTTATGAATAAACAAGGCGGCTTTTTCAGATTAAAGTTGAGAC 838
 Db 878 AAGAATATAAAGTATGTTGCTGCAGAAACAGGTGAGTGTGTTGATAGCAGTAGGTC 937
 QY 839 TCATGGAAGCTGTCTCTCTCTCACACCAGGCAATTCGTTGGTTCCTTTTCATAAATC 898
 Db 938 TCATGAGTGTCTCTGTAATCAAGAAGATTTAAACCGCTACTTAATACACTTGGGC 997
 QY 899 TTTCTGGTATTATTATCAGATTAGAGATGATTAATCTTGAATTTGAAAGATTTCCAAATGT 958
 Db 998 TC-----TTTCCAAATTAGGATGATATGCTAATCT-ACACTCCAAAGATAT 1045
 QY 959 CCAGCGAAAGCTTTGCTGAGGACATTAACAGAGGGAAGTATCTTTTCCATCGTCC 1018
 Db 1046 AGTGAACAAAGTTTGTGAAGATCTGACAGAGGGAAGTTCTCATTTCTACTATTTC 1105
 QY 1019 ACGCCCTT 1026
 Db 1106 ATGCTATT 1113

RESULT 12
 US-10-369-493-27908
 ; Sequence 27908, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 27908
 ; LENGTH: 1284
 ; TYPE: DNA
 ; ORGANISM: Neurospora crassa
 US-10-369-493-27908

Query Match 5.8%; Score 90.6; DB 6; Length 1284;
 Best Local Similarity 49.6%; Pred. No. 7.4e-11;
 Matches 339; Conservative 0; Mismatches 314; Indels 30; Gaps 3;

QY 343 TGGTCCAGCCAAAATGAAGCTTTGATTTTCAAAAACCTTATAATACATCTCTTTTGAACCT 402
 Db 361 TGGTCCGAAGAGAGAGAGAGGTTCTGACGGGTCTTACGACTATCTCAACGGGACCCG 420
 QY 403 GCGAAGACTTTAGACTAAATTTAATAGTTTCAAAATTAACAGAGTTATGAATTTGGCCAAA 462
 Db 421 GGCAGGACATCCGATCGCAGATGTCAGGCTTCGAGCGCTGGCTTGTATGTGCCGTCC 480
 QY 463 GACCAGCTGGCCATAGTTTGCAAAATTTGTAGCTCTTGCATAAATTCAGACCTTTTAAATC 522
 Db 481 GAAAGCTCGAGTATCAACCAAGTCAATCAGCATGCTACACAGACCTCTTGTCTCGTC 540
 QY 523 GACGATATAGAGATAATGCTCCCTTGAGAAAGGAGACAGACCTTCTCACTTAATCTTC 582
 Db 541 GACGACGTGGAAGACAACAGCGTCTTGGCGCCGCGCTTCCCTGTGCCCACTCCATCTTC 600
 QY 583 GGTGTACCTCCACATATAAACCACCAATATATGTAATTTCCAGAGCCATGCAACTTGA 642
 Db 601 GGCATCCCGCAGACCATCAACACGTCCTCAACTACGTGTATTTCTACGCGCTGCAAGATTG 660
 QY 643 TCGCAGCTAAACCAAAAAGAGCGCTTTTGTATCATAATTTGATTACGATTTTCAACGAAGAA 702
 Db 661 CAANAGCTCAAGA-----ACCCCAAGCGCTCAGCATTTTCTCTGAAGAA 705
 QY 703 TTGATCAATCTACATAGAGGACAAAGCTTTGGATATATCTCGAGAGACATTTCTGCTCGAA 762
 Db 706 CTGCTCAACTGCACCGGGCCAGGGAATGGACCTTTTGGCGTGACACGCT-----C 759
 QY 763 ATCATACCTACTCAGAGATGTTTGAATATGTTTGAATAAACAAGCGCGCTTTTC 822
 Db 760 ACTTCCCGCAGGAGACGACTACCTAGAGATGGTATCCAAACAGACAGCGCTCTGTTTC 819
 QY 823 AGATTAAAGCTTCAGACTCATGGAAGCGTGTCTCTCTTCTCACACACCGCCCATTCGTTG 882
 Db 820 CGTTTGGGAATCAAGTGTATGAGCGCGAGTCCGCTCGCGGTGGAGTCG----- 870
 QY 883 GTTCTTTTCAATAATCTTCTGGGTATTAATTAATCAGATTAGAGATGATTACTTTGAATTTG 942
 Db 871 GTCCGCTCGTCAACATCATCGGACTGATCTTCCAGATCGCGAGCATTTATCATATCTG 930
 QY 943 AAAGATTTCCAAATGTCAGCGAAGAAAGCTTTGCTGAGGACATTACAGAGGGGAAGTTA 1002
 Db 931 TGGAAACCGCGATCACCGCCCAACAGGCGATGTGCGAGGACCTGACGGAGGCAAGTTTC 990
 QY 1003 TCTTTTCCCATCGTCCAGCGCCT 1025
 Db 991 AGTTTCCCGTGTATCCACAGCAT 1013

RESULT 13
 US-10-189-268-11
 ; Sequence 11, Application US/10189268
 ; Publication No. US20040005570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas M. Dean
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Kenneth W. Doble
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF GERANYLGERANYL DIPHOSPHATE SYNTHASE 1 EXPR
 ; FILE REFERENCE: PTS-0021
 ; CURRENT APPLICATION NUMBER: US/10/189,268
 ; CURRENT FILING DATE: 2002-07-02
 ; NUMBER OF SEQ ID NOS: 131
 ; SEQ ID NO 11
 ; LENGTH: 51001
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1331-1430, 34714-34813
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-189-268-11


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; SEQ ID NO 21
; LENGTH: 2222
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-041-018-21

Query Match      5.4%; Score 84.2; DB 7; Length 2222;
Best Local Similarity 50.5%; Pred. No. 3.3e-09;
Matches 330; Conservative 0; Mismatches 293; Indels 30; Gaps 4;

QY 374 AACCTTATAATCACATCCCTTTTGAAACCTGGCAAGAACTTTAGACTAAATTTAATAGTTC 433
Db 372 AGCCCTTTACATACACAGATTCTCTGGCAAGCAATTCGCTCTGAGTTGGCCTTG 431
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Db 432 CTTTCAATCACTGGTTGCTCATACCGGGGAAAAGTTGGCGCAGATCGGAGACATTTGTC 491
QY 494 AGCTCTTGCAATATCCAGCCTTTTAAATCGACGATATAGAGATATGCTCCCTTGAGAA 553
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QY 554 GGGGACAGACCACTTCTCACTTAATCTCGGTGTACCTCCACTATAAACAACGCAAAAT 613
Db 552 GAGGTGTCGGCGGCGCATTCATCTACGGCGTGGCCAGCACCATAAATGGGCCAACT 611
QY 614 ATATGTAATTTACAGAGCCATGCAACTTTGTATCGCAGCTAACCAAAAGAGCCCTTTGTATC 673
Db 612 ATGCACCTCTTCTGGCGCTGGAGAAGGTGCAGCAGCTGGATCATCCGGAGGCT----- 664
QY 674 ATAAATTTGATAGATTTTCAACGAGAAATTTGATCAATCTACATAGGGGACAGGCTTGG 733
Db 665 -----ACCAAGGTGTACCCGAAATTTGCTGGAGCTGCACCCGTGGACAGGGCATGG 716
QY 734 ATATATACTGGAGAGACTTCTCGCTGAAATCATACCTACTCAGGAGATGTATTTGAATA 793
Db 717 AGATCTATTGGCGCGACAGCTT-----CACGTGTCATCCGAGTCGGATTACAAGCTGA 770
QY 794 TGGTTATGAATAAAACAGCGCGCTTTTTCAGATTAACGTTGAGACTCATGGAGCGCTGT 853
Db 771 TGACTGTGGCAAAACTGGCGGCTCTTTATGCTGGCCATTCGCCCTTATGCA---GCTGT 827
QY 854 CTCCTTCTCTCACACGCGGCAATTCGTTGGTTCCTTTTCATAAATCTCTGGGTATTTAT 913
Db 828 TCAGCTCCAAACAGGAGGACTATTCGAAG-----TTGACGGCTATATTGGGCCCTGTACT 881
QY 914 ATCAGATTAAGAGATGATTACTTCAATTTGAAGATTTCCAAATGTCCAGCGAAAAAGGCT 973
Db 882 TTCAGATACCGACGACTATTGCAATCTGAGTCTGAAGAGTACACGGAGNACAAGAGCT 941
QY 974 TTGCTCAGGACATTAACAGAGGGGAAGTTATCTTTTCCCATCGTCCACGCCCTT 1026
Db 942 TCGCCGAGGACTTGACGGAGGCAAGTTGGCTTCCCGGTAATCCATCGGGT 994

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Job time : 1358.36 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 06:52:12 ; Search time 163.758 Seconds
(without alignments)
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Title: US-10-041-018-22

Perfect score: 1720

Sequence: 1 MEAKIDELINNPVWSQNE.....DTATNLHDELLYIDHLSL 335

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/abss/ABSSWEB.spool/US10041018/runat_14022006.080431.25006/app_query.fasta_1
-DB=issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
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7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1720	100.0	1005	2	US-08-761-344-1
2	1720	100.0	1569	2	US-08-761-344-3
3	574	33.4	903	2	US-08-469-665-1
4	574	33.4	903	2	US-09-038-596-1
5	574	33.4	903	6	PCT-US95-00421-1
6	538	31.3	1882	3	US-09-091-725-14
7	310.5	18.1	1664976	3	US-08-916-421B-1
8	310.5	18.1	1664976	3	US-09-692-570-1
9	242.5	14.1	924	3	US-09-543-681A-1736

10	234.5	13.6	993	2	US-08-705-377-4	Sequence 4, Appli
11	234.5	13.6	993	2	US-09-052-962-4	Sequence 4, Appli
12	234.5	13.6	993	2	US-09-053-068-4	Sequence 4, Appli
13	233	13.5	1026	3	US-09-252-991A-4877	Sequence 4877, Ap
14	232	13.5	498	3	US-09-248-796A-3882	Sequence 3882, Ap
15	230.5	13.4	993	2	US-08-705-377-3	Sequence 3, Appli
16	230.5	13.4	993	2	US-08-705-377-6	Sequence 6, Appli
17	230.5	13.4	993	2	US-09-052-962-3	Sequence 3, Appli
18	230.5	13.4	993	2	US-09-052-962-6	Sequence 6, Appli
19	230.5	13.4	993	2	US-09-053-068-3	Sequence 3, Appli
20	230.5	13.4	993	2	US-09-053-068-6	Sequence 6, Appli
21	229.5	13.3	993	2	US-08-705-377-5	Sequence 5, Appli
22	229.5	13.3	993	2	US-09-052-962-5	Sequence 5, Appli
23	229.5	13.3	993	2	US-09-053-068-5	Sequence 5, Appli
24	228.5	13.3	990	2	US-08-410-167A-1	Sequence 1, Appli
25	228.5	13.3	993	2	US-08-705-377-1	Sequence 1, Appli
26	228.5	13.3	993	2	US-09-052-962-1	Sequence 1, Appli
27	228.5	13.3	993	2	US-09-053-068-1	Sequence 1, Appli
28	228.5	13.3	993	2	US-08-898-560-2	Sequence 2, Appli
29	228.5	13.3	993	3	US-09-101-126-2	Sequence 2, Appli
30	227	13.2	1029	3	US-09-489-039A-6482	Sequence 6482, Ap
31	225.5	13.1	978	3	US-09-217-609A-4	Sequence 4, Appli
32	225.5	13.1	978	3	US-08-873-235B-4	Sequence 4, Appli
33	225.5	13.1	2451	3	US-09-217-609A-21	Sequence 21, Appl
34	225.5	13.1	2451	3	US-08-873-235B-21	Sequence 21, Appl
35	225	13.1	993	2	US-08-705-377-2	Sequence 2, Appli
36	225	13.1	993	2	US-09-052-962-2	Sequence 2, Appli
37	225	13.1	993	2	US-09-053-068-2	Sequence 2, Appli
38	221.5	12.9	993	3	US-09-252-991A-4908	Sequence 4908, Ap
39	221.5	12.9	1023	3	US-09-543-681A-1606	Sequence 1606, Ap
c 40	211.5	12.3	717	3	US-09-252-991A-4822	Sequence 4822, Ap
c 41	211.5	12.3	1350	3	US-09-266-965-80	Sequence 80, Appl
c 42	211.5	12.3	18034	3	US-09-266-965-75	Sequence 75, Appl
43	210.5	12.2	1219	3	US-09-025-819-28	Sequence 28, Appl
44	210.5	12.2	1219	3	US-09-808-126-28	Sequence 28, Appl
45	210.5	12.2	1219	3	US-09-803-951-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-08-761-344-1

; Sequence 1, Application US/08761344

; Patent No. 5912154

; GENERAL INFORMATION:

; APPLICANT: Ferro-No. 5912154ick, Susan

; APPLICANT: Jiang, Yu

; TITLE OF INVENTION: GERANYLGERANYL DIPHOSPHATE SYNTHASE

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sheridan Ross P.C.

; STREET: 1700 Lincoln Street

; CITY: Denver

; STATE: CO

; COUNTRY: U.S.A.

; ZIP: 80203

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/761,344

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Connell, Gary J.

; REGISTRATION NUMBER: 30,020

; REFERENCE/DOCKET NUMBER: 3161-14

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 303/863-9700

; TELEFAX: 303/862-0223

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1005 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1005
US-08-761-344-1

Alignment Scores:
Pred. No.: 1.08e-194 Length: 1005
Score: 1720.00 Matches: 335
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-041-018-22 (1-335) x US-08-761-344-1 (1-1005)

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QY 21 SerLeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeu 40
DB 61 AGCTTGATTTCAAAACCTTATAATCATCATCCTTTTGAAACCTGGCAAGAACTTTAGACTA 120
QY 41 AsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnIleAlaIleVal 60
DB 121 AATTTAATAGTTCAAAATTAACAGAGTATGAATTTGCCCAAGACAGCTGGCCATAGTT 180
QY 61 SerGlnIleValGluLeuLeuHisSerSerLeuLeuIleAspAspIleGluAspAsn 80
DB 181 TGCAAATTTGTGAGCTCTTGCAATATTCAGCCCTTTTAATCGACATATAGAGTAAAT 240
QY 81 AlaProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIle 100
DB 241 GCTCCCTTCAGAAAGGGGACAGACCACTTCTCACTTAATCTCGGTGACCTCCACTATA 300
QY 101 AsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLys 120
DB 301 AACACGCCAAATTTATATGTTATTTTCAGAGCATGCAACTTTGTATCGCAGTAACCAAAA 360
QY 121 GluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHisArg 140
DB 361 GAGCCTTTGTATCATAAATTTGATTACGATTTTCACGAAAGATTTGATCAATCTACATAGG 420
QY 141 GlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGlnGlu 160
DB 421 GGACAGGCTTGGATATATCTGGAGAGACTTCTGCCTGAAATCATACCTACTCAGGAG 480
QY 161 MetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArgLeu 180
DB 481 ATGTATTTGAATATGCTTTATGAATAAAACAGGGGCGCTTTTCAGATTAACGTTGAGACTC 540
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DB 541 ATGGAAAGCGCTGTCTCCTTCACACCGGCGCATTCGTTGGTTCCTTTCATAAAATCT 600
QY 201 LeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPheGlnMetSer 220
DB 601 CTGGGTATTTATTCAGATTAGAGATGATTACTTCAATTTGAAAGATTTCCAAATGTCC 660
QY 221 SerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHis 240
DB 661 AGCGAAAAAGGCTTCTCGAGGACATTCAGAGGGGAAGTTATCTTTTCCCATCGTCCAC 720
QY 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArgIle 260
DB 721 GCCCTTAACTTCTAATAAAGAAAGGTCAAACTGAGCAACACAAATGAAATTTCTAAGAA 780

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1005 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1005
US-08-761-344-1

Alignment Scores:
Pred. No.: 2.16e-194 Length: 1569
Score: 1720.00 Matches: 335
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-041-018-22 (1-335) x US-08-761-344-3 (1-1569)

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DB 301 ATGGAGGCCAAGATAGATGCTGATCAATATATGATCCTGTTGGTCCAGCCAAATGAA 360
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Qy 21 SerLeuLeuSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeu 40
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Qy 41 AsnLeuLeuValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleVal 60
Db 421 AATTAAATAGTTCAAATTAACAGAGTTATGAATTTGCCCAAAGACCGCTGGCCATAGTT 480
Qy 61 SerGlnIleValGluLeuLeuHisAsnSerSerLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
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Qy 101 AsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrLys 120
Db 601 AACACCCGCAATTAATATATGTTTTCAGAGCCATGCAACTTGTATCGCACTTAACCAAAA 660
Qy 121 GluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuLeuLeuLeuLeuLeu 140
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Db 721 GGACAAGCTTTGGATATATATCTCGAGAGACTTTCTGCTGAAATCATACCTACTCAGGAG 780
Qy 161 MetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuLeuLeuLeuLeuLeu 180
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Qy 221 SerGlnLysGlyPheAlaGluAspIleThrGluLysLeuSerPheProIleValHis 240
Db 961 AGCGAAAAGAGCTTTGCTGAGGACATACAGAGGGAAGTTATCTTTTCCCATCGTCCAC 1020
Qy 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArgIle 260
Db 1021 GCCCTTAACCTTCACTAAACGAAAGGTCAAACTGAGCAACACAAATGAATTTCTAAGAA 1080
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Qy 301 AsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThrAsn 320
Db 1201 AATGATTAATGAAATAATAGTATTTACCTGATTTGGCTTCGATTCGACACCGCCACCAAT 1260
Qy 321 LeuHisAspGluLeuLeuTyrIleIleAspHisLeuSerGluLeu 335
Db 1261 TTACATGCGCAATTTGTTATATATATATAGACCACTTATCCGAAATG 1305
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RESULT 3

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US-08-469-665-1
; Sequence 1, Application US/08469665
; Patent No. 5786193
; GENERAL INFORMATION:
; APPLICANT: GREENE, ET AL.
; TITLE OF INVENTION: Human Geranylgeranyl Pyrophosphate Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,665
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00421
; FILING DATE: 11 JAN 95
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-377
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; US-08-469-665-1
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Alignment Scores:

Pred. No.:	1.81e-58	Length:	903
Score:	574.00	Matches:	127
Percent Similarity:	57.6%	Conservative:	55
Best Local Similarity:	40.2%	Mismatches:	104
Query Match:	33.4%	Indels:	30
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US-10-041-018-22 (1-335) x US-08-469-665-1 (1-903)

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Qy	40	LeuAsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIle	59
Db	85	ACCAAACTTTCACAGGCAATTTAATCATTTGGCTGAAAGTTCCAGAGCAACAGCTACAGATT	144
Qy	60	ValSerGlnIleValGluLeuLeuHisAsnSerSerLeuLeuLeuLeuLeuLeuLeuLeuLeu	79
Db	145	ATTATTGAAGTGCAGAAATGTTGCATAATGCCAGTTTACTCATCGATGATATTGAAGAC	204
Qy	80	AsnAlaProLeuArgArgGlyGlnThrThrSerHisLeuLeuPheGlyValProSerThr	99
Db	205	AACCTAAAACCTCCGACGTGCTTTCCAGTGGCCACACAGCATCTATGGAATCCCATCTGTC	264
Qy	100	IleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThr	119
Db	265	ATCAATTCGCCAATTTACGTGTATTTCTTTGGCTTGGAGAAAGTC-----TTAACCTTT	318
Qy	120	LysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuLeuLeuLeuHis	139
Db	319	GATCACCCTCA-----GATGAGTGAAGCTTTTACCCGCCAGCTTTTGGAACTCCAT	369
Qy	140	ArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGln	159
Db	370	CAGGACAGAGGCTTAGATATTTACTTGGAGGAT-----AATTACACTTGTCTCCCACTGAA	423

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QY 160 GluMetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArg 179
Db 424 GAAGATAATAAGCTATGTGCTGCAGAAACACAGGTGGACTGTTTGGATTACGAGTAGT 483
QY 180 LeuMetGluAlaLeuSerProSerSerHisHisGlyHisSerLeuValProPheLeuAsn 199
Db 484 CTCATGCAGTTGTC-----TCTGATTACAAAGAGATTAAACCGCTACTTAAT 534
QY 200 LeuLeuGlyIleLeuTyrGlnLeuArgAspTyrLeuAsnLeuLysAspPheGlnMet 219
Db 535 ACATCTGGGCTCTTTTCCAAATTAGGGATGATTATGCTAATCTACACTCCAAAGAATAT 594
QY 220 SerSerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleVal 239
Db 595 AGTGAACCAAAAGTTTGGGTGAAGATCTGCACAGAGGAAAGTTCATTTCTCTACTATT 654
QY 240 HisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluLeuArg 259
Db 655 CATGCTATT-----TGTCAAGTCTGAAAGCACCCAGGTGCAGAT 696
QY 260 IleLeuLeuLeuArgThrSerAspLysAspIleLysLeuLysLeuGlnLeuGlu 279
Db 697 ATCTTGGCCAGAGAACAGATAGATATAAAAAAATACCTGTGTACATTCTTTGAG 756
QY 280 PheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeuValAsnMetIle 299
Db 757 ---GATGTAGTTCTGGGAATACACTCGTAATACCTTTAAAGAGCTT----- 801
QY 300 LysAsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThr 319
Db 802 -----GAGCTAAA-----GCCTATAACAGATTGATGCACGT 834
QY 320 AsnLeuHisAspGluLeuLeuTyrIleLeuAspHisLeuSerGluLeu 335
Db 835 GGTGGGAACCTGAGCTAGTACCTTAGTAAACACCTTAAGTAAGATG 882

RESULT 4
US-09-038-596-1
; Sequence 1, Application US/09038596
; Patent No. 5928924
; GENERAL INFORMATION:
; APPLICANT: GREENE, ET AL.
; TITLE OF INVENTION: Human Geranylgeranyl Pyrophosphate Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,596
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,665
; FILING DATE: June 6, 1995
; APPLICATION NUMBER: PCT/US95/00421
; FILING DATE: 11 JAN 95
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-377
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
US-09-038-596-1

Alignment Scores:
Pred. No.: 1,81e-58 Length: 903
Score: 574.00 Matches: 127
Percent Similarity: 57.6% Conservatives: 55
Best Local Similarity: 40.2% Mismatches: 104
Query Match: 33.4% Indels: 30
DB: 2 Gaps: 8

US-10-041-018-22 (1-335) x US-09-038-596-1 (1-903)
QY 20 GluSerLeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArg 39
Db 25 CAAGAAGATCTTCTAGAACCTTATAATACTTACTTACGTTACCCAGGTAAACAAAGTGAGA 84
QY 40 LeuAsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIle 59
Db 85 ACCAACTTTTCACAGGCATTAACTCATTCGCTGAAAGTTCCAGAGGACAAAGCTACAGAT 144
QY 60 ValSerGlnIleValGlnLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAsp 79
Db 145 ATATTGAAGTACAGAAATGTTGCATATGATCCAGTTACTCATCATCATGATATTGAAGAC 204
QY 80 AsnAlaProLeuArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThr 99
Db 205 AACTCAAACTCCGACGTGGCTTCCAGTGGGCCACAGCATCTATGGAATCCCATCTGTC 264
QY 100 IleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThr 119
Db 265 ATCAATTCGCCAATACGTGTATTCTTCGCTGGGAGAAAGTC-----TTAACCCCTT 318
QY 120 LysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHis 139
Db 319 GATCACCCA-----GATGCAGTGAAGCTTTTACCCTCCGACGCTTTTGGAACTCCAT 369
QY 140 ArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleLeuProThrGln 159
Db 370 CAGGGACCAAGGCTAGATATTTACTGGAGGAT-----AATTACACTTGTGCCACTGAA 423
QY 160 GluMetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArg 179
Db 424 GAAGAATATAAGCTATGTGCTGCAGAAACACAGGTGGACTGTTGGATTAGCAGTAGGT 483
QY 180 LeuMetGluAlaLeuSerProSerSerHisHisGlyHisSerLeuValProPheLeuAsn 199
Db 484 CTCATGCAGTTGTC-----TCTGATTACAAAGAGATTAAACCGCTACTTAAT 534
QY 200 LeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPheGlnMet 219
Db 535 ACATCTGGGCTCTTTTCCAAATTAGGGATGATTATGCTAATCTACACTCCAAAGAATAT 594
QY 220 SerSerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleVal 239
Db 595 AGTGAACCAAAAGTTTGGGTGAAGATCTGCACAGAGGAAAGTTCATTTCTCTACTATT 654
QY 240 HisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluLeuArg 259
Db 655 CATGCTATT-----TGTCAAGTCTGAAAGCACCCAGGTGCAGAT 696
QY 260 IleLeuLeuLeuArgThrSerAspLysAspIleLysLeuLysLeuGlnIleLeuGlu 279
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Db 757 ---GATGTAGGTTCTGGGAGATACACTCGTAAATACCTTAAAGAGCTT----- 801
Qy 300 LysAsnAspGluLeuGlnLeuValSerHisSerAspThrAlaThr 319
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Qy 320 AsnLeuHisAspGluLeuValSerHisSerAspGluLeu 335
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RESULT 5

PCT-US95-00421-1

; Sequence 1, Application PC/TUS9500421

; GENERAL INFORMATION:

; APPLICANT: GREENE, ET AL.

; TITLE OF INVENTION: Human Geranylgeranyl Pyrophosphate Synthetase

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/00421

; FILING DATE: Concurrently

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-257

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 903 BASE PAIRS

; TYPE: NUCLEIC ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; MOLECULE TYPE: CDNA

PCT-US95-00421-1

Alignment Scores:

Pred. No.:	1.81e-58	Length:	903
Score:	574.00	Matches:	127
Percent Similarity:	57.6%	Conservative:	55
Best Local Similarity:	40.2%	Mismatches:	104
Query Match:	33.4%	Indels:	30
DB:	6	Gaps:	8

US-10-041-018-22 (1-335) x PCT-US95-00421-1 (1-903)

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Db 25 CAAGAAGATTCTTCTAGAACCTTATAATCTACTTCACTTCAAGTAAACAGTGA 84
Qy 40 LeuAsnLeuLeuValGlnLeuAsnArgValMetAsnLeuProLysAspGlnLeuAla 59
Db 85 ACCAACTTTCACAGGCAATTAATCATTTGGCTGAAAGTTCCAGGAGCAAGCTACAGATT 144
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Qy 100 IleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThr 119
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Qy 140 ArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluLeuIleProThrGln 159
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Qy 320 AsnLeuHisAspGluLeuLeuTyrIleIleAspHisLeuSerGluLeu 335
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RESULT 6

US-09-091-725-14

; Sequence 14, Application US/09091725

; Patent No. 6329141

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Improved methods for transforming Phaffia

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morrison & Foerster llp

; STREET: 2000 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: United States of America

; ZIP: 20006-1888

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible


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OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (1664854)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

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Pred. No.: 4 63e-22 Length: 1664976
Score: 310.50 Matches: 94
Percent Similarity: 44.1% Conservative: 56
Best Local Similarity: 27.6% Mismatches: 119
Query Match: 18.1% Indels: 71
DB: 3 Gaps: 11

US-10-041-018-22 (1-335) x US-08-916-421B-1 (1-1664976)

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QY 20 GluSerLeuIleSerIysProTyrAsn-----HisIleLeuLeuIysProGlyLys 36
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Db 688615 -----GATAAACTATATAACGCGTCAAAACATCTTCTATTTGCTCGAGGAAAG 688662
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Db 688663 AGAATTAGGCCATATTTAACTGTAGTA-----ACTTATATGTTGAAGAAAGACGAT 688713
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QY 57 LeuAlaIleVal-----SerGlnIleValGluLeuLeuHisAsnSerSerLeuLeu 73
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Db 688714 ATTGAGGAGGTTTGGCAGCCGCTGTCAGTAGAGTTAATTCAACACTACACCTTAATA 688773
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QY 74 IleAspAspIleGluAspAsnAlaProLeuArgArgGlyGlnThrThrSerHisLeuIle 93
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Db 688774 CATGATGACATTTATGACAAATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 688833
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QY 94 PheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeu 113
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Db 688834 TATGAGAGCCATGGCTATCTAGCTGGAGATTATATATATGCTAAAGCTTTTGAAGCA 688893
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QY 114 ValSerGlnLeuThrThrIysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGlu 133
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Db 688894 GTTTCAAGAATAAAGATAATAAAGAGCT---CATGAAGTTTAAATAATCTATCAAAA 688950
|||
QY 134 GluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuPro 153
|||
Db 688951 GCATGTTGTAGGTTTGTGAAGGCGAGGCAATGCGCATGGAATTTCAAAACTAC----- 689004
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QY 154 GluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLysThrGlyGlyLeu 173
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Db 689005 -----TATCCTACATGGAAGAACTACTTAGATATGATTAGAAAAAAGACAGAGCTTTA 689058
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QY 174 PheArgLeuThrLeuArgLeuMetGluAlaLeuSerPro---SerSerHisGlyHis 192
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Db 689059 TTAGAGGCTTCGTGGGAATTTGGGCTGTTATGGCTGATTGTAATGAAGAGAAAGGGAA 689118
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QY 193 SerLeuValProPheIleAsnLeuLeuGlyIleIleTyrGlnIleArgAspTyrLeu 212
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Db 689119 GCATTTAAAGAGATATGCAAAAAGAAATTTGGATTAACCTTTTCAAAATACAGGATGTTT 689178
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QY 213 AsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIleThrGluGly 232
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Db 689179 GATTTAATTGGGGACGAGAAAAGTTAGTAAGCCAGTTGGGAAGTGATATAAGAAAGT 689238
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QY 233 LysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGlu 252
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Db 689239 AAAAGACAAATAATGTTATCCAGCC----- 689265
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QY 253 GlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAspIleLysLeu 272
|||
Db 689266 -----CTAAAAACATTTGGATGAAGATAAAGAA 689295
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QY 273 LysLeuIleGlnIleLeu----- 278
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Db 689296 AGATTATTTGGAATTTTAGGAAATAAATAATGTTAGGATGAAGAAATTAAGAACGAATT 689355
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QY 279 GluPheAspThrAsnSerIeuAlaTyrThrIysAsnPheIleAsnGlnIleuValAsnMet 298
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Db 689356 GAGATATTAAAGCCTTCAATTGAATGATGCAAAAGAACTTATGAAAACAAAAAACTGAAGAA 689415
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QY 299 IleLys-----AsnAspAsnGluAsnLysTyrIleuProAspLeuAla 312
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RESULT 8

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US-09-692-570-1
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
; Patent No. 6797466
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (1096846)..(1096846)
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; NAME/KEY: misc feature
; LOCATION: (1130881)..(1130881)
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; NAME/KEY: misc feature
; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g

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Alignment Scores:

Pred. No.:	4,63e-22	Length:	1664976
Score:	310.50	Matches:	94
Percent Similarity:	44.1%	Conservative:	56
Best Local Similarity:	27.6%	Mismatches:	119
Query Match:	18.1%	Indels:	71
DB:	3	Gaps:	11


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US-10-041-018-22 (1-335) x US-09-692-570-1 (1-1664976)
QY 4 LysileAspGlu-----LeuileAsnAsnAspProValTrpSerSerGlnAsn 19
Db 688576 AAAATTGATGAAGAAATTAAGACTTATGTAGATAAAGAT----- 688614
QY 20 GluSerLeuileSerIysProTyrAsn-----HisileuLeuIysProGlyIys 36
Db 688615 -----GATAAACATATATAACGCGTCAAAACATCTTCTATTGCTCGAGGAAG 688662
QY 37 AsnPheArgLeuAsnLeuValGlnileAsnArgValMetAsnLeuProIysAspGln 56
Db 688663 AGAATTAGCCCAATTTAACTAGTA-----ACTTATATGTTGAAGAAAGCAT 688713
QY 57 LeuAlaileVal-----SerGlnileValGluLeuLeuHisAsnSerSerLeuLeu 73
Db 688714 ATTGAGGAGGTTTGGCCAGCGCTGCTGCAGTAGAGTTAATTACAACTACACCTTAATA 688773
QY 74 IleAspAspileGluAspAsnAlaProLeuArgArgGlyGlnThrThrSerHisleuile 93
Db 688774 CATGATGACATTTATGACCAATGATGATGAGAGGAGGAGGAAACCAACAGTTTCTATGTTGTC 688833
QY 94 PheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeu 113
Db 688834 TATGGAGAGCCCAATGGCTATCTTAGCTGGAGATTTATATATGCTTAAAGCTTTTGAAGCA 688893
QY 114 ValSerGlnLeuThrThrIysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGlu 133
Db 688894 GTTTCAGAATAAAGATAAATAAAGCT---CATGAAGTTTAAATAATCTTATCAAAA 688950
QY 134 GluLeuileAsnLeuHisArgGlyGlnGlyLeuAspileTyrTrpArgAspPheLeuPro 153
Db 688951 GCATGTGTGAGGTTTGTGAAGGCGCAGCAATGGACATGGAATTTGAAAACTAC----- 689004
QY 154 GluileileProThrGlnGluMetTyrLeuAsnMetValMetAsnIysThrGlyGlyLeu 173
Db 689005 -----TATCCTACATGGAAGAAATCTTAGATATGATTAGAAAAAAGACAGAGCTTTA 689058
QY 174 PheArgLeuThrLeuArgLeuMetGluAlaLeuSerPro---SerSerHisHisGlyHis 192
Db 689059 TTAGAGGCTTCTGTGGGAATTGGGGCTGTTATGGCTGATTGTAATGAAGAAAGGAA 689118
QY 193 SerLeuValProPheIleAsnLeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeu 212
Db 689119 GCATTAAGAGAGTATGCAAAAAGAAATGGATTAACTTTTCAATATACAGGATGATGTTTAA 689178
QY 213 AsnLeuIysAspPheGlnMetSerSerGluIysGlyPheAlaGluAspileThrGluGly 232
Db 689179 GATTTTAATTGGGACACAGAAAAAGTTAGTAAGCCAGTTGGAAAGTGATATAGAGAAGGT 689238
QY 233 LysLeuSerPheProIleValHisAlaLeuAsnPheThrIysThrIysGlyGlnThrGlu 252
Db 689239 AAAAGACAAATAATTGTTATCCAGCC----- 689265
QY 253 GlnHisAsnGluileLeuArgIleLeuLeuLeuLeuLeuLeuSerAspIysAspileIysLeu 272
Db 689266 -----CTAAAAACATTTGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 689295
QY 273 LysLeuileGlnIleLeu----- 278
Db 689296 AGATTATGGAAATTTTAGGAAATAAAATGTTAAGGATGAAGAAATTAAGAAAGCAATT 689355
QY 279 GluPheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeuValAsnMet 298
Db 689356 GAGATATTAAAGCTTCAATTGATATGCAAAAGAACTTATGAAACAAAACCTGAAGAA 689415
QY 299 IleLys-----AsnAspAsnGluAsnLysTyrIleAsnProAspLeuAla 312
Db 689416 GCAAAAGAAATATTAAAGATATTCAATATAAGACAGAAGGAAAGTTTTATAGAGGATTTGGCT 689475

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RESULT 9

US-09-543-681A-1736

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; Sequence 1736, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 1736
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1736

Alignment Scores:
Pred. No.: 4,99e-19 Length: 924
Score: 242.50 Matches: 77
Percent Similarity: 47.2% Conservative: 67
Best Local Similarity: 25.2% Mismatches: 132
Query Match: 14.1% Indels: 29
DB: 3 Gaps: 8

US-10-041-018-22 (1-335) x US-09-543-681A-1736 (1-924)
QY 4 LysileAspGluLeuileAsnAsnAspProValTrpSerSerGlnAsnGluSerLeuile 23
Db 61 CTGTGTGATGAAGCACTCAACCAAGCGCTACAAACGTTCCCTTTCTCATATGCCACTC 120
QY 24 SerLysProTyrAsnHisIleleuLeuIysProGlyIysAsnPheArgLeuAsnleuile 43
Db 121 AGCCAAAGCAATGCGTACGAGCACTCTTGGGGGGGAAACGTTTACGCCCATTTCTCGTT 180
QY 44 ValGlnileAsnArgValMetAsnLeuProIysAspGlnLeuAlaileValSerGlnile 63
Db 181 TATGCGGTAGGAGAAATGTTTAACTGTTGCTTAATCTTGATGTGCCAGCGCGCT 240
QY 64 ValGluLeuLeuHisAsnSerSerLeuLeuileAspAspileGlu-----AspAsnAla 81
Db 241 ATTGATGTATTATCATGTCATATTCTACCTGATCCATCAGCACTTACCTGCAATGGACAATGAT 300
QY 82 ProLeuArgArgGlyGlnThrThrSerHisleuilePheGlyValProSerThrIleAsn 101
Db 301 GATTTACGTCGAGGAAACCCACTTGTCTATATTGAGTTTGGCGAAGCCCAATGCCATTTTA 360
QY 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGlu 121
Db 361 GCGGGTGTGATGCAATTAACAACTTTGGCCTTTGAAATTTTAGCCAAAAAATGGGATGCTGAT 420
QY 122 ProLeuTyrHisAsnLeuileThrIlePheAsnGlu-----GluLeuile 136
Db 421 CTCGCCATTGGCCGATCGCTAGCCATGATTGCTGAATTAGCCACAGCAGTGGTTTAGCG 480
QY 137 AsnLeuHisArgGlyGlnGlyLeuAspileTyrTrpArgAspPheLeuProGluileile 156
Db 481 GGTATGTGTGTGTCGACAGGCACTTGTATCTTGTATGTCGCGAAGATAAAATCAATTTGATCTGTC 540
QY 157 ProThrGlnGluMetTyrIleAsnMetValMetAsnLysThrGlyGlyLeuPheArgLeu 176
Db 541 GCTCTTTGAGAAATTCATTTA-----CATAAACACAGTGGCTGTTAATTCGTGCA 588
QY 177 ThrLeuArgLeuMetGluAlaLeuSerProSerHisHisSerLeuValPro 196
Db 589 GCGGTTTCGCTA---CGGGCACTTAC---GCAGGCGCAAAAGGCGCACGATGTTTACCT 642
QY 197 -----PheIleAsnLeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeu 212
Db 643 GCACCTGGATAAAATATGCCACTCTATAGGCTTTCCAAAGTTCCAGGTATGATTTTA 702
QY 213 AsnLeuIysAspPheGlnMetSerSerGluIysGlyPheAlaGluAspileThrGluGly 232

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Db 703 GATGTTATTGGGAGCACTGAAGAGACTGGAAAGCGACAGGGAAGTGATCAAGAAGCTGGA 762
 Qy 233 LysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGlu 252
 Db 763 AAAAGTACTTATCCGGCTCTACTTGGTTAGCAACAAGCACAAGAAAGCACAG--GAA 819
 Qy 253 GlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAspIleLysLeu 272
 Db 820 TTGTATAACGAAGCATTTGGAT-----GCTTAA 846
 Qy 273 LysLeuIleGlnLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsnPheIle 292
 Db 847 GCGTTTCTTGAACAATACGAGTACGATACCTCTACGCTAAACAATTAAGCGAATTTATC 906
 Qy 293 AsnGlnLeuValAsn 297
 Db 907 GTAGAACGGGAAAC 921

RESULT 10

US-08-705-377-4
 ; Sequence 4, Application US/08705377
 ; Patent No. 5807725
 ; GENERAL INFORMATION:
 ; APPLICANT: OHTO, Chikara, ASADA, Chika, OHNUMA, Shinichi,
 ; APPLICANT: NISHINO, Tokuzo, HIROOKA, Kazutake, HEMMI, Hisashi
 ; TITLE OF INVENTION: Long-Chain Prenyl Diphosphate Synthase
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kenyon & Kenyon
 ; STREET: 1025 Connecticut Avenue, N.W., Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20036

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch Diskette
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 6.1 Windows
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/705,377
 ; FILING DATE: 29-AUG-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 7247043
 ; FILING DATE: 01 SEP 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Toffenetti, Judith L.
 ; REGISTRATION NUMBER: 39,048
 ; REFERENCE/DOCKET NUMBER: 77670/442
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-429-1776
 ; TELEFAX: 202-429-0796
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 993
 ; TYPE: Nucleic acid
 ; STRANDEDNESS: Double strand
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: Mutated genomic DNA

US-08-705-377-4

Alignment Scores:
 Pred. No.: 4,99e-18 Length: 993
 Score: 234.50 Matches: 84
 Percent Similarity: 46.3% Conservative: 65
 Best Local Similarity: 26.1% Mismatches: 150
 Query Match: 13.6% Indels: 23
 DB: 2 Gaps: 10

US-10-041-018-22 (1-335) x US-08-705-377-4 (1-993)

Qy 6 AspGluLeuIleAsnAsn---AspProValTrpSerSerGlnAsnGluSerLeuIleSer 24
 Db 25 AATGAGATTGTTAATCTGTAACAGCATATTATTAAAGAGCTATATATCTGGAGATGTTCTT 84
 Qy 25 LysProTyrAsn-----HisIleLeuLeuLysProGlyLysAsnPheArgLeuAsn 41
 Db 85 AAATCTATATGAAGCCTCATATCATCTCTGGAGGTAAAGAGTTAAAGACCATTA 144
 Qy 42 LeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleValSer 61
 Db 145 ATCTTAACATATATCATCAGATTATTTCGGAGGACAGAGAGAAAGAGCTTATTATGCGAGT 204
 Qy 62 GlnIleValGlnLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAspAsnAla 81
 Db 205 GCAGCTATTGAAGTCTTCTCATCTTCTACGCTTGTCATCATGATATATGATCAAGAT 264
 Qy 82 ProLeuArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsn 101
 Db 265 AATATCAGAAGAGGGTTACCCACAGTCCAGTCAATACGGCTTACCTTACGCAATATTA 324
 Qy 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGlu 121
 Db 325 GCTGGGGATTACTACATCAAGGGCTTTTACGCTCTTAACCCAGGCTCTTAGAGGTTTG 384
 Qy 122 Pro-----LeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHis 139
 Db 385 CCAAGTGAAACCATTAATTAAGGCTTTTCGATATTTTCACTCGTTCATAATAATATATATCC 444
 Qy 140 ArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGln 159
 Db 445 GAAGCAGCAGGCGATAGATATGAATTTGAGGACAGAAATTCAT-----ATAAAGGAGCAG 498
 Qy 160 GluMetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArg 179
 Db 499 GAA---TACCTTGACATGATCTCACGTAAGCAGAGTGCATATTATCTCGGCATCTCAAGT 555
 Qy 180 LeuMetGluAlaLeuSerProSerHisHisGlyHisSerLeuVal---ProPheIle 198
 Db 556 ATAGGCGCACTTATGCTGGTGTCTAATGATGATGATGATGATGATGATGATGATGATGAT 615
 Qy 199 AsnLeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPheGln 218
 Db 616 ACGAATCTAGGTATTGCAATTCAGATTGTTGACGATATCTTAGCTCTTAACAGCAGACGAA 675
 Qy 219 MetSerSerGluLysGlyPheAlaGluAspIleThrGluLysLeuSerPheProIle 238
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 Qy 239 ValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeu 258
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 Qy 259 ArgIleLeuLeuLeuArgThrSerAspLysAspIleLysLeuLysLeuIleGlnIleLeu 278
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 Qy 279 GluPheAspThrAsnSerLeuAlaTyrThr-----LysAsnPheIle 292
 Db 844 AAGAAATACTCTTTTAGATTATGATACAAATTTAGCAGAGAAATATTATATAAAATGCTATA 903
 Qy 293 AsnGlnLeuValAsnMetIle-----LysAsnAspAsnGluAsnLysTyrLeuProAsp 310
 Db 904 GACTCTTTA---AATCAAGTCTCTCTAGAGGTATATACCTCGGAAGGGCTTTAAATAT 960
 Qy 311 LeuAla 312
 Db 961 CTAGCT 966

RESULT 11

US-09-052-962-4
 ; Sequence 4, Application US/09052962
 ; Patent No. 5882909
 ; GENERAL INFORMATION:

APPLICANT: OHTO, Chikara, ASADA, Chika, OHNUMA, Shinichi,
 APPLICANT: NISHINO, Tokuzo, HIROOKA, Kazutake, HEMMI, Hisashi
 TITLE OF INVENTION: Nucleic Acid Encoding Mutant
 TITLE OF INVENTION: Geranylgeranyl Diphosphate Synthase
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenyon & Kenyon
 STREET: 1025 Connecticut Avenue, N.W., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20036

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch Diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 6.1 Windows
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/052,962
 FILING DATE: Concurrent Herewith
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/705,377
 FILING DATE: 29-AUG-1996
 APPLICATION NUMBER: JP 7247043
 FILING DATE: 01 SEP 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Toffenetti, Judith L.
 REGISTRATION NUMBER: 39,048
 REFERENCE/DOCKET NUMBER: 77670/545
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-429-1776
 TELEFAX: 202-429-0796

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 993
 TYPE: Nucleic acid
 STRANDEDNESS: Double strand
 TOPOLOGY: Linear
 MOLECULE TYPE: Mutated genomic DNA
 US-09-052-962-4

Alignment Scores:
 Pred. No.: 4,99e-18 Length: 993
 Score: 234.50 Matches: 84
 Percent Similarity: 46.3% Conservative: 65
 Best Local Similarity: 26.1% Mismatches: 150
 Query Match: 13.6% Indels: 23
 DB: 2 Gaps: 10

US-10-041-018-22 (1-335) x US-09-052-962-4 (1-993)

QY 6 AspGluLeuLeuAsnAsn---AspProValTyrSerSerGlnAsnGluSerLeuLeuSer 24
 Db 25 AATGAGATTGTTAATCTCTTAACGACATATTAAGAGCTATATCTCGAGATGTTCT 84
 QY 25 LysProTyrAsn-----HisLeuLeuLysProGlyLysAsnPheArgLeuAsn 41
 Db 85 AAACATATGAAGCCTCATATCTTTTACATCTGGAGGTTAAGAGCCATTA 144
 QY 42 LeuLeuValGlnLeuAsnArgValMetAsnLeuProLysAspGlnLeuAlaValSer 61
 Db 145 ATCTTAATATATCATCATGATTATTTCGGAGGACAGAGAAAGAGCTTTATTGCGAGT 204
 QY 62 GlnLeuValGlnLeuLeuHisAsnSerSerLeuLeuLeuAspLeuGluAsnAla 81
 Db 205 GCAGCTATTGAGTCTTCTACTCTTCTAGCTTGCTGATGATATTAATGATCAAGAT 264
 QY 82 ProLeuArgArgGlyGlnThrThrSerHisLeuLeuPheGlyValProSerThrLeuAsn 101
 Db 265 AATATCAGAAGAGGGTTACCCACAGCCACGTCAGTAAATACGGCTTACCTTAGCAATATTA 324
 QY 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGlu 121

Db 325 GCTGGGATTTACTACATGCAAGGCTTTTACGCTCTTAACCCAGGCTCTTAGAGGTTTG 384
 QY 122 Pro-----LeuTyrHisAsnLeuLeuThrLeuPheAsnGluGluLeuLeuAsnLeuHis 139
 Db 385 CCAAGTGAAACCATAAATAAGGCTTTTCGATATTTTCTACGTTCAATAATAATTATATCC 444
 QY 140 ArgGlyGlnGlyLeuAspLeuTyrTrpArgAspPheLeuProGluLeuLeuLeuProThrGln 159
 Db 445 GAAGGACAGCGCATAGATATGAATTTGAGGAGCAAGATTGAT-----ATAAGGAGCAG 498
 QY 160 GluMetTyrLeuAsnMetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeuArg 179
 Db 499 GAA---TACCTTGACATGATCTCAGTAGACAGAGCTGCATTAATTCGCGCATCTCAAGT 555
 QY 180 LeuMetGluAlaLeuSerProSerSerHisHisGlyHisSerLeuVal---ProPheLeu 198
 Db 556 ATAGGCGCACTTATTGCTGGTCTTAATGATATGATGTAAGACTGATGCTGATTTCCGGT 615
 QY 199 AsnLeuLeuGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 218
 Db 616 ACGAATCTAGGTATTGCAATTTTCAGATTGTTGACGATATCTTAGGCTTAACAGCAGCGAA 675
 QY 219 MetSerSerGluLysGlyPheAlaGluAspLeuThrGluGlyLysLeuSerPheProIle 238
 Db 676 AAGGAACCTTGGAAAGCCTGTTTATTAGTATATAGGAGGTTAAAGAGACTATATCTGTA 735
 QY 239 ValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluLeu 258
 Db 736 ATAAAAACACCTGGAGCTTTGTAAA-----GAGGACGAGAGAAGATTGTCCTA 783
 QY 259 ArgIleLeuLeuLeuArgThrSerAspLysAspIleLysLeuLysLeuLeuGlnIleLeu 278
 Db 784 AAGGCGTTAGGTAAATAAGTCAGCTCAAAAGAGAATAATTAATGAGCTCAGCAGATATAAT 843
 QY 279 GluPheAspThrAsnSerLeuAlaTyrThr-----LysAsnPheLeu 292
 Db 844 AAGAAATCTCTTTAGATTATGATACATATTTAGCAGAGAAATATTTATAAAATGCTATA 903
 QY 293 AsnGlnLeuValAsnMetIle-----LysAsnAspAsnGluAsnLysTyrLeuProAsp 310
 Db 904 GACTCTTTA---AATCAAGTCTCTCTTAAGAGTGATATACCTGGAAAGGCTTTAAAAATAT 960
 QY 311 LeuAla 312
 Db 961 CTAGCT 966
 RESULT 12
 US-09-053-068-4
 Sequence 4, Application US/09053068
 Patent No. 5885810
 GENERAL INFORMATION:
 APPLICANT: OHTO, Chikara, ASADA, Chika, OHNUMA, Shinichi,
 APPLICANT: NISHINO, Tokuzo, HIROOKA, Kazutake, HEMMI, Hisashi
 TITLE OF INVENTION: Process for The Production of Prenyl
 TITLE OF INVENTION: Diphosphate and Mutants Thereof
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kenyon & Kenyon
 STREET: 1025 Connecticut Avenue, N.W., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch Diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 6.1 Windows
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/053,068
 FILING DATE: Concurrent Herewith
 CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,377
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: JP 7247043
; FILING DATE: 01 SEP 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-1776
; TELEFAX: 202-429-0796
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993
; TYPE: Nucleic acid
; STRANDEDNESS: Double strand
; TOPOLOGY: Linear
; MOLECULE TYPE: Mutated genomic DNA
US-09-053-068-4

Alignment Scores:
Pred. No.: 4.99e-18 Length: 993
Score: 234.50 Matches: 84
Percent Similarity: 46.3% Conservative: 65
Best Local Similarity: 26.1% Mismatches: 150
Query Match: 13.6% Indels: 23
DB: 2 Gaps: 10

US-10-041-018-22 (1-335) x US-09-053-068-4 (1-993)

QY 6 AspGluLeuLeuAsnAen---AppProValTrpSerSerGlnAenGluSerLeuLeuSer 24
DB 25 AATGAGATTGTAATTCGTAACGACATTAATTAAGAGCTATATATCTGGAGATGTTCT 84
QY 25 LysProTyrAen-----HisLeuLeuLysProGlyLysAenPheArgLeuAen 41
DB 85 AAATATATGAGCCTCATATCATTTCTTACATCTCGAGGTAAGAGTTAAGACCATTA 144
QY 42 LeuLeuValGlnLeuAenArgValMetAenLeuProLysAenGlnLeuAlaValSer 61
DB 145 ATCTTAATCATATCATGAGTTTATTCGAGGACAGAGAGAGAGCTTATTATGCAGGT 204
QY 62 GlnLeuValGluLeuLeuHisAenSerSerLeuLeuLeuAspAspLeuGluAenAenA 81
DB 205 GCAGCTATTGAGTCTTCACTTCTACCTTGTGATGATGATATATGATGATCAAGAT 264
QY 82 ProLeuArgArgGlyGlnThrThrSerHisLeuLeuPheGlyValProSerThrLeuAen 101
DB 265 AATATCAGAGAGGGTTACCCACAGTCCAGTGAATACGGCTTACCTTAGCAATATTA 324
QY 102 ThrAlaAenTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGlu 121
DB 325 GCTGGGGATTACTACATGCAAGGGCTTTTCAGCTCTTAACCCAGGCTCTTAGAGGTTG 384
QY 122 Pro-----LeuTyrHisAenLeuLeuThrLeuPheAenGluLeuLeuAenLeuHis 139
DB 385 CCAAGTGAACCAATAAATAGGCTTTCGATATTTCACTCGTTCAATAATAATATATCC 444
QY 140 ArgGlyGlnGlyLeuAenPheLeuTyrTrpArgAenPheLeuProGluLeuLeuProThrGln 159
DB 445 GAAGGACAGGAGTATGATATGATATGATGATGATGATGATGATGATGATGATGATGAT 498
QY 160 GluMetTyrLeuAenMetValMetAenLysThrGlyGlyLeuPheArgLeuThrLeuArg 179
DB 499 GAA---TACCTTGACATGATCTCAGTAAGAGAGTGCATATTTCTCGGATCCTCAAGT 555
QY 180 LeuMetGluAlaLeuSerProSerSerHisGlyHisSerLeuVal---ProPheLeu 198
DB 556 ATAGGGCCCATTTATGCTGTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 615
QY 199 AsnLeuLeuGlyLeuLeuTyrGlnLeuArgAenAspTyrLeuAenLeuLysAenPheGln 218

DB 616 ACGAATCTAGGTATTGCAATTTTCAGATTGTTGACGATATCTTAGGTCTTAACAGCAGACGAA 675
QY 219 MetSerSerGluLysGlyPheAlaGluAspLeuThrGluGlyLysLeuSerPheProIle 238
DB 676 AAGGAACCTTGGAAAGCCTGTTTATGATATATTAGGAGGGTAAAGAGACTATCTACTGTA 735
QY 239 ValHisAlaLeuAenPheThrLysThrLysGlyGlnThrGluGlnHisAenGluLeuLeu 258
DB 736 ATAAACACACTGGAGCTTTGTA---GAGGACGAGAGAAGATTGTCCTA 783
QY 259 ArgLeuLeuLeuLeuArgThrSerAspLysAspLeuLysLeuLeuGlnLeuLeu 278
DB 784 AAGCGTGTAGGTAATAAGTCAGCTCAAAAGAGAATAATAGCTCAGCAGATATAAT 843
QY 279 GluPheAspThrAenSerLeuAlaTyrThr-----LysAenPheIle 292
DB 844 AAGAAATACCTTTTAGATTATGATACAAATTTAGCAGAGAAATATTATAAAATGCTATA 903
QY 293 AsnGlnLeuValAenMetIle-----LysAenAspAenGluAenLysTyrLeuProAen 310
DB 904 GACTCTTA---AATCAAGTCTCTCTAAGAGTGATATACCTGGAAGGGCTTTAAATAT 960
QY 311 LeuAla 312
DB 961 CTAGCT 966

RESULT 13

US-09-252-991A-4877
; Sequence 4877, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4877
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4877

Alignment Scores:
Pred. No.: 7.92e-18 Length: 1026
Score: 233.00 Matches: 65
Percent Similarity: 48.2% Conservative: 81
Best Local Similarity: 21.5% Mismatches: 135
Query Match: 13.5% Indels: 22
DB: 3 Gaps: 6

US-10-041-018-22 (1-335) x US-09-252-991A-4877 (1-1026)

QY 22 LeuLeuSerLysProTyrAenHisIleLeuLeuLysProGlyLysAenPheArgLeuAen 41
DB 148 CTGGTGGAAAGATCGCGACTACATCATCTCCGCGCGGCAAGCGCTCGCGCGCTG 207
QY 42 LeuLeuValGlnLeuAenArgValMetAenLeuProLysAenGlnLeuAlaValSer 61
DB 208 CTGGTCTGCTCGCGCAAGACCTTGGGCTACAGGCGGACGACCTCTGCTGCTGCC 267
QY 62 GlnLeuValGluLeuLeuHisAenSerSerLeuLeuLeuAspAspLeuGluAenAenA 81
DB 268 GCACCATCGAATCTCTGACACCTCACTCTGCTGACGACGAGCTGTCGACGCTCC 327
QY 82 ProLeuArgArgGlyGlnThrThrSerHisLeuLeuPheGlyValProSerThrLeuAen 101
DB 328 GGCTGCGCGCGCGCTCCACCGCAATGCTGTGGGGCAAGCGCGCGGCTGCTGCTG 387

QY 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGlu 121
 Db 388 GTAGGCGACTCTTTATCGCCGCTCTTCGAATATGCTGAGCTGGTTCATCGCG 447
 QY 122 ProLeuTyrHisAsnLeuThrThrPheAsnGluGluLeuLeuAsnLeuHisArgGly 141
 Db 448 -----GTCATGGCGCATATATCCAGCCACCGCGGTGATCGCCGAGGCG 492
 QY 142 GlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGlnGluMet 161
 Db 493 GAAGTGCTCAATG-----TCCAAGGTACGGACGCCAGCACTACCGAGAGACC 543
 QY 162 TyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArgLeuMet 181
 Db 544 TACATGGAAGTGTATCGCGCGCAAGACCGATGCTTTTCGAGCGCTTCGACCCACAGCGCC 603
 QY 182 GluAlaLeu--SerProSerHisHisGlyHisSerLeuValProPheIleAsnLeu 200
 Db 604 GCGCGCTGTGCCAGCGCGGAGGAGACAGTCCGAGGCACTGCGCGCTTCGCGGACTAC 663
 QY 201 LeuGlyIleIleTyrGlnIleArgAspTyrLeuAsnLeuLysAspPheGlnMetSer 220
 Db 664 CTGGGAATCGCTTCAGCTGTGGAGCACTCTGCTACCGCGCGGACCGCGGACC 723
 QY 221 SerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHis 240
 Db 724 CTGGCAAGAAGCTCGCGGACGACCTCGCGGAGGCAAGCAACCCACCTACCGCTGATCGTC 783
 QY 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArgIle 260
 Db 784 ACATG-----CGTGACGGCACCGGAGGAGCGCGCTGTGTACGCAAG 828
 QY 261 LeuLeuLeuArgThrSerAspLysAspIleLys-----LeuLysLeuIle 275
 Db 829 GCCATCCAGACGGCGGACCGGACGACCTGGAGAGCGTGTGTCCGCCCTCGAGGCTGCC 888
 QY 276 GlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeu 295
 Db 889 GCGCGCTCGGATATACCGCCCAAC-----CTGCGCGCGGACTACCGCGCGCGCC 939
 QY 296 ValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSerHisSer 315
 Db 940 ATCGCTCGCTGGATACGCTGCGGACCAAGATACCGCTCGCGCCCTGTGTGAACTCAGC 999
 QY 316 AspThrAla 318
 Db 1000 GAATTCGCT 1008

RESULT 14
 US-09-248-796A-3882
 ; Sequence 3882, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 3882
 ; LENGTH: 498
 ; TYPE: DNA
 ; ORGANISM: Candida albicans
 US-09-248-796A-3882
 Alignment Scores: 3.39e-18 Length: 498
 Pred. No.:

Score: 232.00 Matches: 67
 Percent Similarity: 53.3% Conservative: 30
 Best Local Similarity: 36.8% Mismatches: 57
 Query Match: 13.5% Indels: 28
 DB: 3 Gaps: 8
 US-10-041-018-22 (1-335) x US-09-248-796A-3882 (1-498)
 QY 162 TyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArgLeuMet 181
 Db 10 TATTTGGAAATGATTAAGATAAACTGGTGGTGTTCAGATTGGCAATTAATTTG 69
 QY 182 GluAlaLeuSerProSerSerHisHisGlyHisSerLeuValProPheIleAsnLeu 201
 Db 70 CTGTTGTATTCAGATGTACAGAAAC---GATCAATTAATATCCCTTCGCAATTAATG 126
 QY 202 GlyIleIleTyrGlnIleArgAspTyrLeuAsnLeuLysAspPheGlnMetSerSer 221
 Db 127 GGCATTTTGTATCAAGTTAGACGCGATTAATTTGAATTTAGTGGATGCCAAGTATTCTCGC 186
 QY 222 GluLysGly---PheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHis 240
 Db 187 ATGAAAGGCACATACATGTGAGACTTGATAGAGGAGGAAAGTTATCATTCCTATATTACAT 246
 QY 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArgIle 260
 Db 247 TGTCTAAGAACCACTAAG-----GATTCACTGTACACAAATA 285
 QY 261 LeuLeuLeuArgThrSerAspLysAsp-----IleLysLeuLys 273
 Db 286 CTATATGATTACGACTCTAGCTCCGATCGTGTTCCTCAAAATCTTTAATTCATTAAGT 345
 QY 274 LeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsn 293
 Db 346 TTA---AGCTTTATGAAATAAGTCCAAATCTTTGGAGTATACATGAATTAATTAAG 402
 QY 294 GlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSer 313
 Db 403 GTATTGGAAAGAAATTAAGA---CAATTGATTTTGAAGTAT---CCTGAGCTGGAGAAC 456
 QY 314 HisSerAspThrAlaThrAsnLeuHisAspGluLeuLysTyrIleIleAspHisLeuSer 333
 Db 457 TCTGCA-----TTATTGAAATTTGTTGACGCTTTATGT 489
 QY 334 GluLeu 335
 Db 490 GATCTT 495
 RESULT 15
 US-08-705-377-3
 ; Sequence 3, Application US/08705377
 ; Patent No. 5807725
 ; GENERAL INFORMATION:
 ; APPLICANT: OHTO, Chikara, ASADA, Chika, OHNUMA, Shinichi,
 ; APPLICANT: NISHINO, Tokuzo, HIROOKA, Kazutake, HEMMI, Hisashi
 ; TITLE OF INVENTION: Long-Chain Prenyl Diphosphate Synthase
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kenyon & Kenyon
 ; STREET: 1025 Connecticut Avenue, N.W., Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch Diskette
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 6.1 Windows
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/705,377
 ; FILING DATE: 29-Aug-1996
 ; CLASSIFICATION: 435

Search completed: February 16, 2006, 08:15:55
Job time : 721.758 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 07:57:49 ; Search time 726.582 Seconds
(without alignments)
3812.705 Million cell updates/sec

Title: US-10-041-018-22

Perfect score: 1720

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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-DB=Published Applications NA_Main -OFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100

-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEASize=500 -MINLEN=0

-MAXLEN=200000000 -HOST=abes04

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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main:

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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1720	100.0	1008	6	US-10-369-493-46181
2	1720	100.0	1008	7	US-10-450-941-5
3	1720	100.0	1563	7	US-10-041-018-1
4	974	56.6	599	9	US-10-487-901-363
5	629.5	36.6	1044	6	US-10-369-493-36092
6	623	36.2	1284	6	US-10-369-493-27908
7	584	34.0	1395	6	US-10-189-268-4

8	584	34.0	1692	3	US-09-814-353-21762	Sequence 21762, A
9	584	34.0	2534	7	US-10-041-018-3	Sequence 3, Appli
10	577	33.5	2529	3	US-09-925-302-171	Sequence 171, App
11	577	33.5	2529	3	US-09-925-302-171	Sequence 171, App
12	545.5	31.7	2210	10	US-11-097-143-9632	Sequence 9632, Ap
13	545.5	31.7	2222	7	US-10-041-018-21	Sequence 21, Appl
14	541.5	31.5	1364	6	US-10-369-493-36669	Sequence 36669, A
15	538	31.3	1882	7	US-10-001-192A-14	Sequence 14, Appl
16	537.5	31.2	1888	8	US-10-357-930-25125	Sequence 25125, A
17	525.5	30.6	51001	6	US-10-189-268-11	Sequence 11, Appl
18	488.5	28.4	1843	7	US-10-041-018-5	Sequence 5, Appli
19	475.5	27.6	961	6	US-10-369-493-36678	Sequence 36678, A
20	395	23.0	716	3	US-09-969-034-1924	Sequence 1924, Ap
21	380	22.1	912	6	US-10-369-493-36606	Sequence 36606, A
22	374.5	21.8	7837	7	US-10-041-018-2	Sequence 2, Appli
23	370	21.5	6977	10	US-11-097-143-9631	Sequence 9631, Ap
24	357.5	20.8	935	6	US-10-369-493-36350	Sequence 36350, A
25	337	19.6	1044	7	US-10-282-122A-10905	Sequence 10905, A
26	310.5	18.1	984	6	US-10-369-493-45179	Sequence 45179, A
27	305.5	17.8	554	3	US-09-969-034-1324	Sequence 1324, Ap
28	290.5	16.9	593	3	US-09-969-034-1488	Sequence 1488, Ap
29	278.5	16.2	1095	7	US-10-282-122A-40388	Sequence 40388, A
30	246.5	14.3	966	7	US-10-282-122A-32007	Sequence 32007, A
31	243.5	14.2	972	7	US-10-282-122A-42025	Sequence 42025, A
32	242.5	14.1	921	7	US-10-282-122A-32509	Sequence 32509, A
33	239	13.9	978	6	US-10-369-493-24788	Sequence 24788, A
34	238.5	13.9	975	7	US-10-282-122A-29902	Sequence 29902, A
35	238.5	13.9	2242716	9	US-10-915-740A-1068	Sequence 1068, Ap
36	236	13.7	972	7	US-10-282-122A-29211	Sequence 29211, A
37	234	13.6	966	6	US-10-369-493-37633	Sequence 37633, A
38	233	13.5	969	3	US-09-815-242-7933	Sequence 7933, Ap
39	233	13.5	969	7	US-10-282-122A-30502	Sequence 30502, A
40	228.5	13.3	966	7	US-10-282-122A-33315	Sequence 33315, A
41	227	13.2	963	7	US-10-282-122A-15089	Sequence 15089, A
42	226.5	13.2	930	6	US-10-369-493-43383	Sequence 43383, A
43	226	13.1	972	7	US-09-815-242-9636	Sequence 9636, Ap
44	226	13.1	972	7	US-10-282-122A-38868	Sequence 38868, A
45	226	13.1	972	7	US-10-282-122A-39465	Sequence 39465, A

ALIGNMENTS

RESULT 1

US-10-369-493-46181
; Sequence 46181, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 46181
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-46181

Alignment Scores:
Pred. No.: 3 58e-181
Score: 1720.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 6
Length: 1008
Matches: 335
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

Db 541 ATGGAAGCGTGCTCTCTCCACACACCGGCATTCGTTGGTCTCTTTCATATAATCTT 600
Qy 201 LeuGlyLeuThrGlnLeuAspGlyLeuAsnLeuLysAspPheGlnMetSer 220
Db 601 CTGGTAT 660
Qy 221 SerGlyLeuPheAlaGluAspPheThrGluGlyLysLeuSerPheProIleValHis 240
Db 661 AGCGAAAAAGCGTTCTGCTAGGACATTTACAGAGGGAAGTTATCTTTTCCCATCGTCCAC 720
Qy 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisGlnGluLeuArgIle 260
Db 721 GCCTTTAACTTCACTAAACGAAAGGTCAAACTGAGCAACACCAATGAAATTTCTAAGAATT 780
Qy 261 LeuLeuLeuArgThrSerAspLysAspPheLeuLysLeuLeuGlnLeuGluPhe 280
Db 781 CTCTGTTGAGGCAAGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 840
Qy 281 AspThrAsnSerLeuAlaTyrThrLysAsnGlnPheIleAsnGlnLeuValAsnMetIleLys 300
Db 841 GACACCAATTCATTTGGCTACACCAAAAATTTTATTAATCAATAGTAGTGAATGATAAAA 900
Qy 301 AsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThrAsn 320
Db 901 AATGATAATGAAATAAGTATTTACCTGATTTGGCTTCGCATTCGACACCGCCACCAAT 960
Qy 321 LeuHisAspGluLeuLeuTyrIleLeuAspHisLeuSerGluLeu 335
Db 961 TTACATGACGAATTTGTTATATATAATAGACCACTTATCCGAATTTG 1005

RESULT 3

US-10-041-018-1

; Sequence 1, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; CURRENT APPLICATION NUMBER: US/10/041,018
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-041-018-1

Alignment Scores:

Pred. No.: 7.27e-181 Length: 1569
Score: 1720.00 Matches: 335
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-041-018-22 (1-335) x US-10-041-018-1 (1-1569)

Qy 1 MetGluAlaLysIleAspGluLeuIleAsnAsnAspProValTrpSerSerGlnAsnGlu 20
Db 301 ATGGAGGCCAAGATAGATGATGATCAATTAATGATCCTGTTGGTCCAGCCAAAATGAA 360
Qy 21 SerLeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeu 40
Db 361 AGCTTGATTTCAAAACCTTATAATCATCATCTTTTGAACCTGGCAGAACTTTAGACTA 420
Qy 41 AsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleVal 60
Db 421 AATTTAATAGTTCAATTAACAGATTATGAATTTGCCCAAGACCGAGCTGGCCATAGTT 480

Qy 61 SerGlnIleValGluLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAsn 80
Db 481 TCGCAATTTGTTGAGCTCTTGCATATATTCAGGCTTTTATTCGACGATATAGAATAAT 540
Qy 81 AlaProLeuArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIle 100
Db 541 GCTCCCTTGGAGAGGGGACAGACCCTTCTCACTTAATCTTCGGTGTGACCTCCACTATA 600
Qy 101 AsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLys 120
Db 601 AACCCGCAAAATATATATATTTTCAGAGCCATGCAACTTGTATCGCAGCTAACCAAAA 660
Qy 121 GluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHisArg 140
Db 661 GAGCCTTTGTATCATTAATTTGATTACGATTTTCAACGAAGAATTCATCAATCTACATAGG 720
Qy 141 GlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGlnGlu 160
Db 721 GGACAAAGGCTTGGATATATATCTGGAGAGACTTTCTGCCTGAAATCATACCTACTCAGGAG 780
Qy 161 MetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArgLeu 180
Db 781 ATGTATTTGAATATGTTATGTAATAAACAGCGGCGCTTTTCAGATTAACTTGAGACTC 840
Qy 181 MetGluAlaLeuSerProSerSerHisHisGlyHisSerLeuValProPheIleAsnLeu 200
Db 841 ATGGAAGCGCTGCTCTCTCTCCACACCGGCATTCGTTGGTCTCTTTCATAAATCTT 900
Qy 201 LeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPheGlnMetSer 220
Db 901 CTGGGTATTATTTATCAGATTAGATGATTACTTGAATTTGAAAGATTTTCCAAATGTCC 960
Qy 221 SerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHis 240
Db 961 AGCGAAAAAGGCTTGTCTGAGGACATTTACAGAGGGGAAGTTATCTTTTCCCATCGTCCAC 1020
Qy 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArgIle 260
Db 1021 GCCCTTAACTTCACTAAACGAAAGGTCAAACTGAGCAACACCAATGAAATTTCTAAGAATT 1080
Qy 261 LeuLeuLeuArgThrSerAspLysAspIleLysLeuLysLeuIleGlnIleLeuGluPhe 280
Db 1081 CTCTCTGTTGAGGACAAAGTGAATAAGATATAAAACTAAAGCTGATTCAAACTACTGGAATTC 1140
Qy 281 AspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeuValAsnMetIleLys 300
Db 1141 GACACCAATTCATTTGGCCTACACCAAAAATTTTATTAATCAATTAGTGAATATGATATA 1200
Qy 301 AsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThrAsn 320
Db 1201 AATGATAATGAATAAATAGTATTTTACCTGATTTGGCTTCGCATTTCCGACCCGCCACCAT 1260
Qy 321 LeuHisAspGluLeuLeuTyrIleIleAspHisLeuSerGluLeu 335
Db 1261 TTACATGACGAATTTGTTATATATAATAGACCACTTATCCGAATTTG 1305

RESULT 4

US-10-487-901-363
; Sequence 363, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crossley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteristic

```

; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 363
; LENGTH: 599
; TYPE: DNA
; ORGANISM: saccharomyces cerevisiae
US-10-487-901-363

```

Alignment Scores:		
Pred. No.:	2.54e-98	Length:
Score:	974.00	Matches:
Percent Similarity:	97.9%	Conservative:
Best Local Similarity:	97.4%	Mismatches:
Query Match:	56.6%	Indels:
DB:	9	Gaps:
		599
		188

US-10-041-018-22 (1-335) x US-10-487-901-363 (1-599)

Qy	1	MetGluAlaIysIleAspGluLeuIleAsnAsnAspProValTrpSerSerGlnAsnGlu	20
Db	19	ATGGAGCCAAACATACATGAGCTGATCAATATGATCTCTGTGTGGCCAGCAAAATGAA	78
Qy	21	SerLeuIleSerIysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeu	40
Db	79	AGCTTGATTTCAAAACCTTATATACATCTCTTTTGAACCTTGGCAAGACTTTAGACTA	138
Qy	41	AsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleVal	60
Db	139	AATTTAATAGTTCAAATTAACAGAGTATGAATTTGCCCAAGACCAGCTGGCCATAGTT	198
Qy	61	SerGlnIleValGluLeuLeuHisIleAsnSerSerLeuLeuIleAspAspIleGluAspAsn	80
Db	199	TCGCAAAATTTGTTGAGCTCTTGCACTAATTTCCAGCCTTTTAATCGACGATATAGAAGATAAT	258
Qy	81	AlaProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIle	100
Db	259	GCTCCCTTGAGAAGGGGACAGACCACCTTCTCACTTAATCTTCGGTGATACCCCTCCACTATA	318
Qy	101	AsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrls	120
Db	319	AACACCCGGAATATATATGATGATTTTCAGAGCATGCAACTTGTATCGAGCTAACCCACAAAA	378
Qy	121	GluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHisArg	140
Db	379	GAGCCCTTGTATCATAAATTTGATTAACAATTTTCAACGAAAAATTGATCAATCTCATAGG	438
Qy	141	GlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGlnGlu	160
Db	439	GGCAAGAGCTTGATATATACCTGGAGAGACTTTCTTCGCTGAAATCATACCTTACTCAGGAG	498
Qy	161	MetTyrLeuAsnMetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeuArgLeu	180
Db	499	ATGATTTTGAATATGTTATGAATATAAACAGCGCGCCCTTTTCAGATTAACTGTGAGACTC	558
Qy	181	MetGluAlaLeuSerProSerSerHisIleGlyHisSer	193
Db	559	ATGGAACACTGTCTCTCTCTCTCACACAGCGGCATTGCG	597

RESULT 5

US-10-369-493-36092
; Sequence 36092, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES


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QY 50 MetAsnLeuProLysAspGlnLeuAlaIleValSerGlnIleValGluLeuLeuHisAsn 69
DB 284 CTGAAGTTCCAGAGGACAGCTATATTATTGAATGACAGAAATGTTGCATAAT 343
QY 70 SerSerLeuLeuLeaAspIleGluAspAsnAlaProLeuArgArgGlyGlnThrThr 89
DB 344 GCAGTTTACTCATGATGATATTGAAGCAACTCAAACTCGAGCTGGCTTCCAGTG 403
QY 90 SerHisLeuIlePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArg 109
DB 404 GCCCAGCATCTATGGAATCCCACTGTCATCAATCTGCAATACGTGATTTCCYT 463
QY 110 AlaMetGlnLeuValSerGlnLeuThrThrLysGluProLeuTyrHisAsnLeuIleThr 129
DB 464 GCGTTTGGAGAAAGTC-----TTAACCTTGTATCACCCA-----GATGCGAGTGAAG 508
QY 130 IlePheAsnGluGluLeuLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArg 149
DB 509 CTTTTTACCCGCGAGCTTTTGAACCTCCATCAGGGACAAGGCTAGATATTTACTGGAGG 568
QY 150 AspPheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLys 169
DB 569 GAT-----AATTACACTTGTCCCACTGAAGAAGATATAAAGCTATGCTGCAGAAA 622
QY 170 ThrGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerSerHis 189
DB 623 ACAGGTGGACTGTTGGATTAGCAGTAGCTCTCATGCAGTTGTTCT-----TCTGAT 673
QY 190 HisGlyHisSerLeuValProPheIleAsnLeuGlyIleIleTyrGlnIleArgAsp 209
DB 674 TACAAAGAAGATTAAACCGCTACTTAATACACTGGGCTCTTTTCCAAATTAGGGAT 733
QY 210 AspTyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIle 229
DB 734 GATTATGCTAATCTACACTCCAAGAAATATAGTGAACAAAGTTTGTGAAGATCTG 793
QY 230 ThrGluGlyLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGly 249
DB 794 ACAGAGGGAAGATTCTCATTTCTACTATTCTGCTATT-----TGG 835
QY 250 GlnThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAsp 269
DB 836 TCAAGGCTTGAAGACCCAGGTGCGAATATCTTGGCCGACAGAACAAACATAGAT 895
QY 270 IleLysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLys 289
DB 896 ATAAAAAATACTGTGTACATTATCTTGAG--GATGTAGGTCTTTTCAATACACTCGT 952
QY 290 AsnPheIleAsnGlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuPro 309
DB 953 AATACCTTAAAGAGCTT-----GAGCTAAA-----979
QY 310 AspLeuAlaSerHisSerAspThrAlaThrAsnLeuHisAspGluLeuLeuTyrIleIle 329
DB 980 -----GCCATAAACAGATTGATGCAGCTGGTGGGAACCCGAGCTAGTACGCTTAGTA 1033
QY 330 AspHisLeuSerGluLeu 335
DB 1034 AAACACTTAAGTAAGATG 1051

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RESULT 8

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US-09-814-353-21762
; Sequence 21762, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-0068

```

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; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21762
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1692
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-21762

```

```

Alignment Scores:
Pred. No.: 4,27e-54 Length: 1692
Score: 584.00 Matches: 130
Percent Similarity: 57.7% Conservative: 58
Best Local Similarity: 39.9% Mismatches: 106
Query Match: 34.0% Indels: 32
DB: 3 Gaps: 9

```

US-10-041-018-22 (1-335) x US-09-814-353-21762 (1-1692)

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QY 12 AspProValTrpSerSerGlnAsn-----GluSerLeuIleSerLysProTyrAsnHis 29
DB 249 AATCCAATGGAGAGACCTCAAGAAACAGTCCAAAGAAATTTCTTAGAACCCCTATAAATAC 308
QY 30 IleLeuLeuLysProGlyLysAsnPheArgLeuAsnLeuIleValGlnIleAsnArgVal 49
DB 309 TTACTTTCAGTACAGGTAAACAAGTGAGAACCAACTTTCACAGGCATTTAATCATTTGG 368
QY 50 MetAsnLeuProLysAspGlnLeuAlaIleValSerGlnIleValGluLeuLeuHisAsn 69
DB 369 CTGAAGTTCCAGAGGACAAAGCTACAGATTATTATTGAAGTCACAGAAATGTTGCATAAT 428
QY 70 SerSerLeuLeuIleAspAspIleGluAspAsnAlaProLeuArgArgGlyGlnThrThr 89
DB 429 GCGAGTTTACTCATGATGATATTGAAGCAACTCAAACTCCGACGTGGCTTCCAGTG 488
QY 90 SerHisLeuIlePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArg 109
DB 489 GCCCAGCATCTATGGAATCCCACTGTCATCAATCTGCAATACGTGATTTCCYT 548
QY 110 AlaMetGlnLeuValSerGlnLeuThrThrLysGluProLeuTyrHisAsnLeuIleThr 129
DB 549 GCGTTTGGAGAAAGTC-----TTAACCTTGTATCACCCA-----GATGCGAGTGAAG 593
QY 130 IlePheAsnGluGluLeuLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArg 149
DB 594 CTTTTTACCCGCGAGCTTTTGAACCTCCATCAGGGACAAGGCTAGATATTTACTGGAGG 653
QY 150 AspPheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLys 169
DB 654 GAT-----AATTACACTTGTCCCACTGAAGAAGATATAAAGCTATGCTGCAGAAA 707
QY 170 ThrGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerSerHis 189
DB 708 ACAGGTGGACTGTTGGATTAGCAGTAGTCTCATGCAGTTGTTCT-----TCTGAT 758
QY 190 HisGlyHisSerLeuValProPheIleAsnLeuLeuGlyIleIleTyrGlnIleArgAsp 209

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Db 759 TACAAAGAGATTAAACCGCTACTTAATACACTTGGGCTCTTTTCCAAATTAGGAT 818
Qy 210 AspTyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIle 229
Db 819 GATTATGCTAATCTACACTCCAAAGAAATATAGTGAAACAAAAGTTTTTGTGAAGATCTG 878
Qy 230 ThrGluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGly 249
Db 879 ACAGAGGGAAGTCTCAATCTTCTACTATTTCATGCTATT-----TGG 920
Qy 250 GlnThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuLeuArgThrSerAspLysAsp 269
Db 921 TCAAGGCTCAAGACCCAGGTGCAGAAATATCTTGGCCAGAGAACAGAAAACATAGAT 980
Qy 270 IleLysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLys 289
Db 981 ATAAATAAAATPACTGTGTACATTATCTTGAG---GATGTAGGTTCTTTTGAATACACTCGT 1037
Qy 290 AsnPheIleAsnGlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuPro 309
Db 1038 AATACCTTAAGAGCTT-----GAGCTAAA----- 1064
Qy 310 AspLeuAlaSerHisSerAspThrAlaThrAsnLeuHisAspGluLeuLeuTyrIleIle 329
Db 1065 -----GCCTATAACAGATTGATGCACGTTGGTGGGAACCTGAGCTAGTAGCTTAGTA 1118
Qy 330 AspHisLeuSerGluLeu 335
Db 1119 AAACACTTAAGTAAGATG 1136

RESULT 9
US-10-041-018-3
; Sequence 3, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080U1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Human
US-10-041-018-3

Alignment Scores:
Pred. No.: 8.15e-54 Length: 2534
Score: 584.00 Matches: 130
Percent Similarity: 57.7% Conservative: 58
Best Local Similarity: 39.9% Mismatches: 106
Query Match: 34.0% Indels: 32
DB: Gaps: 9

US-10-041-018-22 (1-335) x US-10-041-018-3 (1-2534)

Qy 12 AspProValTyrSerSerGlnAsn-----GluSerLeuLysSerLysProTyrAsnHis 29
Db 227 AATCCATGTGAGAGACTCAAGAAACAGTCCAAAGAAATCTTCTAGAACCCCTATAATAC 286
Qy 30 IleLeuLysLysProGlyLysAsnPheArgLeuAsnLeuValGlnIleAsnArgVal 49
Db 287 TTATTCAGTTACAGGTAAACAAAGTGCAGAACCAACTTTCACAGGCAATTAATCATGG 346
Qy 50 MetAsnLeuProLysAspGlnLeuAlaIleValSerGlnIleValGluLeuLeuHisAsn 69
Db 347 CTGAAAGTTCCAGAGGCAAGCTACAGATTATTATTGAAGTGCAGAGAAATGTTGCATAAT 406
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Qy 70 SerSerLeuLeuIleAspAspIleGluAspAsnAlaProLeuArgArgGlyGlnThrThr 89
Db 407 GCAGTTTACTCATCGATGATATTTGAAGACACTCAAAACTCCGACCTGGCTTCCAGTG 466
Qy 90 SerHisLeuIlePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArg 109
Db 467 GCCACACAGCACTCATGAATCCCATCTGTCAATCAATCTGCAATTAACGTATTTCTCT 526
Qy 110 AlaMetGlnLeuValSerGlnLeuThrLysGluProLeuTyrHisAsnLeuLeuThr 129
Db 527 GGCTTGGAGAAAGTC-----TTAACCTTGTACCCCA-----GATGCAGTAGAAG 571
Qy 130 IlePheAsnGluGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTyrArg 149
Db 572 CTTTTTACCCGCCAGCTTTTGGAACTCCATCAGGACAGCCCTAGATATATTACTGGAGG 631
Qy 150 AspPheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLys 169
Db 632 GAT-----AATTACACTTGTCCCACTGAAGAAAGATATAAAGCTATGGTGTCTGCAGAA 685
Qy 170 ThrGlyGlyLysLeuArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerSerHis 189
Db 686 ACAGGTGGACTGTTGGATTAGCAGTAGGTCTCATCGAGTTGTTTC-----TCTGAT 736
Qy 190 HisGlyHisSerLeuValProPheIleAsnLeuLeuGlyIleIleTyrGlnIleArgAsp 209
Db 737 TACAAGAAGATTAAACCGCTACTTAAATACACTTGGGCTCTTTTCCAAATTAGGAT 796
Qy 210 AspTyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIle 229
Db 797 GATTATGCTAATCTACACTCCAAAGAAATATAGTGAAACAAAAGTTTTTGTGAAGATCTG 856
Qy 230 ThrGluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGly 249
Db 857 ACAGAGGGAAGTCTCATTTCTTCTACTATTTCATGCTATT-----TGG 898
Qy 250 GlnThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAsp 269
Db 899 TCAAGGCTCAAGACCCAGGTGCAGAAATATCTTGGCCAGAGAACAGAAAACATAGAT 958
Qy 270 IleLysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLys 289
Db 959 ATAAAAAATACTGTGTACATTATCTTGAG---GATGTAGGTTCTTTTGAATACACTCGT 1015
Qy 290 AsnPheIleAsnGlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuPro 309
Db 1016 AATACCTTAAAGAGCTT-----GAAAGCTAAA----- 1042
Qy 310 AspLeuAlaSerHisSerAspThrAlaThrAsnLeuHisAspGluLeuLeuTyrIleIle 329
Db 1043 -----GCCTATAACAGATTGATGCACGTTGGTGGGAACCCCTGAGCTAGTAGCCTTAGTA 1096
Qy 330 AspHisLeuSerGluLeu 335
Db 1097 AAACACTTAAGTAAGATG 1114

RESULT 10
US-09-925-302-171
; Sequence 171, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 171
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-302-171

Alignment Scores:
Pred. No.: 4.9e-53 Length: 2529
Score: 577.00 Matches: 129
Percent Similarity: 57.4% Conservatives: 58
Best Local Similarity: 39.6% Mismatches: 107
Query Match: 33.5% Indels: 32
DB: Gaps: 9

US-10-041-018-22 (1-335) x US-09-925-302-171 (1-2529)

QY 12 AspProValTrpSerSerGlnAsn-----GluSerLeuIleSerLysProTyrAsnHis 29
DB 215 AATCCAAATGGAGAGACTCAAGAAACAGTCCAAAGAAATCTCTAGAACCCCTATAAATAC 274
QY 30 IleLeuLeuLysProGlyLysAsnPheArgLeuAsnLeuValGlnIleAsnArgVal 49
DB 275 TTACTTTCAGTACCAGGTAACCAAGTGAGAACCAAACTCCAGCGTGGCTTTCAGTGG 334
QY 50 MetAsnLeuProLysAspGlnLeuAlaIleValSerGlnIleValGlnLeuLeuHisAsn 69
DB 335 CTGAAAGTTCCAGAGGACCAAGCTACAGATTATTATGAAGTACAGAAATGTTGCATAAT 394
QY 70 SerSerLeuLeuIleAspAspIleGluAspAsnAlaProLeuArgArgGlyGlnThr 89
DB 395 GCCAGTTTACTCATCGATGATATTGAAGACAACTCAAAACCTCCGAGCTGGCTTTCAGTG 454
QY 90 SerHisLeuIlePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArg 109
DB 455 GCCCAGAGCATCTATGGAATCCCATCTGTCATCAATCTGCCAATTACGTGATTTCCCTT 514
QY 110 AlaMetGlnLeuValSerGlnLeuThrLysGluProLeuTyrHisAsnLeuIleThr 129
DB 515 GCGTTGGAGAAAGTC-----TTAACCCCTTGATCACCCA-----GATGCGAGTGAAG 559
QY 130 IlePheAsnGlnGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArg 149
DB 560 CTTTATACCCGCGCAGCTTTTGGAACTCCATCAGGACCAAGGCTAGATATTACTGGAGG 619
QY 150 AspPheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLys 169
DB 620 GAT-----AATTACACTTGTCCCACTGAAGAAGATATAAAGCTATGCTGTCAGAGAA 673
QY 170 ThrGlyGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerHis 189
DB 674 ACAGGTGGAAGTGTGTGGATTAGCAGTAGCTCTCATGCTGCTGCTGCTGCTGCTGCTGCT 724
QY 190 HisGlyHisSerLeuValProPheIleAsnLeuGlyIleIleTyrGlnIleArgAsp 209
DB 725 TCAAAAGAAGATTAAACCGCTACTTAAATACACTTGGGCTCTTTTCCAAATTTAGGAT 784
QY 210 AspTyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIle 229
DB 785 GATTATGCTAATCTACACTCCAAAGAAATATAGTGAAACCAAAAGTTTKGTGAAGATCTG 844
QY 230 ThrGluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGly 249
DB 845 ACAGAGGGAAGAGTCTCATTTCCCTACTATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 886
QY 250 GlnThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAsp 269
DB 887 TCAGGYCTGAAGACACCGGTCGAGATATCTCCGCGAGAGAACCAATAGATAGAT 946
QY 270 IleLysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLys 289
DB 947 ATAAAAAATACTGTGTACATTATCTTGAG---GATGTAGGTTCTTTTGAATACACTCGT 1003
QY 290 AsnPheIleAsnGlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuPro 309
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Db 494 GCTTCATTGCT-GTAGGCTCTTTCCACCTCACCACCAACCACTCCAGTTCAGACAGATT 552
Qy 74 -----ileAspAspIleGluAspAsnAlaProLeuArgArgGly 86
Db 553 GACAAATTTGTGACGCGAGATATCGAGACTACTCCAAACTCCGCGCGGC 612
Qy 87 GlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsnThrAlaAsnTyrMet 106
Db 613 TTCCTCTGCGCACACAGCATCTTCGGCATTCGCGAGACATCAACTCTGCTAACTACGCC 672
Qy 107 TyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGluProLeuTyrHisAsn 126
Db 673 TACTTCCAGCACAGACGAGGCTGTAATTCGCGAGATCGGAG-----AAA 720
Qy 127 LeuIleThrIlePheAsnGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIle 146
Db 721 GCCTTACGTATCTTTACAGAGGAGCTTCTCGGCTGCACAGAGCCAGGGAATGGATCTC 780
Qy 147 TyrTrpArgAspPheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetVal 166
Db 781 TACTGGAGGATTCCTCTC-----ACCTGCCCACTGAAGAGGAGTACCTGGACATGGTG 834
Qy 167 MetAsnLysThrGlyGlyLeuPheArgLeuThrLeuArgLeuMet----- 181
Db 835 GCAAAACAAGACGGCGGGCTTTTTCGGCTCGCCATTAAAGCTTATTCAGTTGGAAAGTGAC 894
Qy 182 -----GluAlaLeuSerPro 186
Db 895 GTTGATGAGTTCGGCGCCTCTTGAGTTTCTTCATATTATTTAGACAGAGCTGAACAGA 954
Qy 187 SerSerHisHisGlyHisSerLeuValProPheIleAsnLeuGlyIleIleTyrGln 206
Db 955 CTTCATTACGG-CCGAGGACTGGCTCCCTAGTAGGACCTGCTAGGTATATCTTCAG 1013
Qy 207 IleArgAspAspTyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAla 226
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Qy 227 GluAspIleThrGluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLys 246
Db 1074 GAGGACATACAGAGGCAAGTCTCTACCCGATGTCCATAGTATTCGAAGTAGCAGT 1133
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Qy 286 AlaTyrThrLysAsnPheIleAsnGlnLeu 295
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RESULT 15

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US-10-001-192A-14
; Sequence 14, Application US/10001192A
; Publication No. US20040091958A1
; GENERAL INFORMATION:
; APPLICANT: Oeljen, Albert
; APPLICANT: Verdoes, Jan
; APPLICANT: Wery, Jan
; TITLE OF INVENTION: IMPROVED METHODS FOR TRANSFORMING
; TITLE OF INVENTION: PHAFFIA STRAINS, TRANSFORMED PHAFFIA STRAINS SO OBTAINED AND
; FILE OF INVENTION: RECOMBINANT DNA IN SAID METHODS
; FILE REFERENCE: 24615-20104.01
; CURRENT APPLICATION NUMBER: US/10/001.192A
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: EP 95203620.0
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: EP96200943.7
; PRIOR FILING DATE: 1996-04-11
; NUMBER OF SEQ ID NOS: 57
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; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 14
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Phaffia rhodozyma
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1212)
US-10-001-192A-14
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Alignment Scores:
Pred. No.: 6.85e-49 Length: 1882
Score: 538.00 Matches: 117
Percent Similarity: 52.1% Conservative: 79
Best Local Similarity: 31.1% Mismatches: 110
Query Match: 31.3% Indels: 70
DB: 7 Gaps: 7
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US-10-041-018-22 (1-335) x US-10-001-192A-14 (1-1882)
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Qy 35 GlyLysAsnPheArgLeuAsnLeuIleValGlnIleAsnArgValMetAsnLeuProLys 54
Db 181 GGAAGAATAATTCGATCACAACATCATCGAGGCTTCAACTATTGGTTGGATGTCAAGAG 240
Qy 55 AspGlnLeuAlaIleValSerGlnIleValGluLeuLeuHisAsnSerSerLeuLeuIle 74
Db 241 GAGGATCTCGAGGTCATCCAGAACGTTGTTGGCATGCTACATACCTACCTAGCTTATTATG 300
Qy 75 AspAspIleGluAspAsnAlaProLeuArgArgGlyGlnThrThrSerHisLeuIlePhe 94
Db 301 GAGGATGTGGAGGATTCATCGGTCCTCAGCGGGGGTGGCTGTGCGCCCATCTAATTTAC 360
Qy 95 GlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuVal 114
Db 361 GGGATTCGGCAGACAAATAACACTGCAAACTAGCTCTACTTTCTGGCTTATCAAGAGATC 420
Qy 114 ----- 114
Db 421 TTCAAGCTTCGCCCAACACCGATACCCATCCCTGTAATTCCTCCTCATCTGCTTCGCTT 480
Qy 114 ----- 114
Db 481 CAATCATCCGCTCTCTCTGTCATCCTCTCTCTCGGCCCTCTGCTGAAAAAGGGGGCAGC 540
Qy 115 -----SerGlnLeuThrThrLysGluProLeuTyrHisAsnLeuIleThrIle 130
Db 541 TCAACTCCTTAATTCGAGATTCGTTCTCGAAAGATACGTAT-----CTTGATAAAGTG 594
Qy 131 PheAsnGluGluLeuLeuAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArgAsp 150
Db 595 ATCAGACAGCAGATGCTTCCCTCCATAGAGGGCAAGGCTCGAGCTATTCTCGAGAGAT 654
Qy 151 PheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLysThr 170
Db 655 AGTCTG-----ACGTGTCCTACGAGAGAGAAATATGTGAAATGGTTCCTTGGAAAGACG 708
Qy 171 GlyGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerSerHisHis 190
Db 709 GGAAGTTTGTTCGTATAGCGGTACAGTTGATGATGCA-----AAGTCAGATGT 759
Qy 191 GlyHisSerLeuValProPheIleAsnLeuGlyIleIleTyrGlnIleArgAspAsp 210
Db 760 GACATAGACTTGTCCAGCTTGTCAACTGATCTCAATATATCTCCAGATCAGGAGATGAC 819
Qy 211 TyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIleThr 230
Db 820 TATATGAACCTTCAGTCTTCTGAGTATGCCCAATAATAAGAAATTTTCAGAGGACCTCACA 879
Qy 231 GluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGlyGln 250
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Db      880 GAAGGAAATTCAAGTTTCCCACTCCCACTCGAATTCAGCCCAACCCCTCATCG----- 933
Qy      251 ThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAspIle 270
Db      934 -----AGACTCGTCATCAATACGTTGCAGAAGAATCGACCTCTCCTGAGATC 981
Qy      271 LysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsn 290
Db      982 CTTCAACCACTGTGTAAACTACATGCGCACAGAAACCCACTCATTCGAATATATCTCAGGAA 1041
Qy      291 PheIleAsnGlnLeuValAsnMetIleLysAsnAsp----- 302
Db      1042 GTCTCAACACCTTGTCAAGGTGCACCTCGAGAGAGAACTAGGAAGGCTTCAAGGAGAGTTC 1101
Qy      303 -----AsnGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThr 319
Db      1102 GCAGAGAGCTAACTCAAGGATGGATCTTGGAGACGTAGATTTCGAAGGAAGAACGGGGAAG 1161
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Db      1162 AACGTC-----AAATTGGAAGCGATCTCGAAAAAGCTAGCCGATATC 1203

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Search completed: February 16, 2006, 10:49:52
Job time : 733.562 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 05:56:03 ; Search time 271.703 Seconds
(without alignments)
10264.856 Million cell updates/sec

Title: US-10-041-018-1

Perfect score: 1569

Sequence: 1 aatattacatatagatag.....aatcgcggttaattcgga 1569

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
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- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1005	64.1	1005	2	US-08-761-344-1
3	114	7.3	903	2	US-08-469-665-1
4	114	7.3	903	2	US-09-038-596-1
5	114	7.3	903	6	PCT-US95-00421-1
6	70.6	4.5	1882	3	US-09-091-725-14
7	65	4.1	498	3	US-09-248-796A-3882
8	52.6	3.4	832	3	US-09-621-576-2813
9	49.8	3.2	1141	3	US-09-806-708B-22
10	48.2	3.1	1664976	3	US-08-916-421B-1
11	48.2	3.1	1664976	3	US-09-692-570-1
12	45.2	2.9	392000	3	US-10-027-983-11
13	44.8	2.9	486	3	US-09-248-796A-3883
14	44.6	2.8	50000	3	US-09-662-254B-26
15	43	2.7	1055	3	US-09-806-708B-23
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17	42.8	2.7	1141	3	US-09-806-708B-22
18	42.2	2.7	222691	3	US-09-949-016-11762
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20	42	2.7	54461	3	US-09-949-016-16411
21	42	2.7	56700	3	US-09-949-016-12573
22	41.6	2.7	385136	3	US-09-949-016-16073
23	41.2	2.6	19438	3	US-09-949-016-12699
24	41	2.6	765	3	US-09-601-198-160

Sequence 1, Appli
Sequence 1, Appli
Sequence 14209, A
Sequence 13614, A
Sequence 16600, A
Sequence 171661, A
Sequence 171662, A
Sequence 2, Appli
Sequence 4, Appli
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Sequence 4, Appli
Sequence 4, Appli
Sequence 8427, App
Sequence 14164, A
Sequence 179, App
Sequence 573, App
Sequence 720, App
Sequence 12053, A
Sequence 12721, A
Sequence 15692, A

25 40.8 2.6 1956 3 US-08-559-896B-1
26 40.8 2.6 1956 3 US-09-351-794A-1
27 40.6 2.6 83210 3 US-09-949-016-14209
28 40.6 2.6 183202 3 US-09-949-016-13614
29 40.6 2.6 298336 3 US-09-949-016-16600
30 40.2 2.6 601 3 US-09-949-016-171661
31 40.2 2.6 601 3 US-09-949-016-171662
32 40 2.5 993 2 US-08-705-377-2
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37 40 2.5 993 2 US-09-053-068-4
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39 39.8 2.5 6388 3 US-09-573-080A-179
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41 39.6 2.5 52174 3 US-09-949-002-573
42 39.6 2.5 52289 3 US-09-949-002-720
43 39.4 2.5 87352 3 US-09-949-016-12053
44 39.4 2.5 87352 3 US-09-949-016-12721
45 39.4 2.5 87352 3 US-09-949-016-15692

ALIGNMENTS

RESULT 1
US-08-761-344-3
; Sequence 3, Application US/08761344
; Patent No. 5912154
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yu
; APPLICANT: Ferro-No. 5912154ick, Susan
; TITLE OF INVENTION: GERANYLGERANYL DIPHOSPHATE SYNTHASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,344
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 30,020
; REFERENCE/DOCKET NUMBER: 3161-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/862-0223
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-761-344-3

Query Match 100.0%; Score 1569; DB 2; Length 1569;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db
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661 GAGCCTTTGTATCAATTAATTTAGTATGATTTTCAACGAAAGATTTGATCAATCTACATAG 720
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Db 1441 TCTCTTAGTTTCGCAAAATAGTCAAAATCTTCAAATTTTATAGCCTTTATATTTTTCACGAT 1500
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QY 1561 AATTCGCGA 1569
Db 1561 AATTCGCGA 1569
RESULT 2
US-08-761-344-1
; Sequence 1, Application US/08761344
; Patent No. 5912154
; GENERAL INFORMATION:
; APPLICANT: Ferro-No. 5912154ick, Susan
; APPLICANT: Jiang, Yu
; TITLE OF INVENTION: GERANYLGERANYL DIPHOSPHATE SYNTHASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,344
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 30,020
; REFERENCE/DOCKET NUMBER: 3161-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/862-0223
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1005 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single


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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1005
; US-08-761-344-1

Query Match      64.1%; Score 1005; DB 2; Length 1005;
Best Local Similarity 100.0%; Pred. No. 1.9e-246; Indels 0; Gaps 0;
Matches 1005; Conservative 0; Mismatches 0;

Qy 301 ATGAGGCCAAGATAGATGAGTCAATTAATGATCCTGTTGGTCCAGCCAAATGAA 360
Db 1 ATGAGGCCAAGATAGATGAGTCAATTAATGATCCTGTTGGTCCAGCCAAATGAA 60

Qy 361 AGCTTGATTTCAAACTTATATACATCCTTTTGAACCTGCGAAGACTTTAGACTA 420
Db 61 AGCTTGATTTCAAACTTATATACATCCTTTTGAACCTGCGAAGACTTTAGACTA 120

Qy 421 AATTTAATAGTTCAAATTAACAGAGTTATGAATTTGCCAAAGACAGCTGGCCATAGTT 480
Db 121 AATTTAATAGTTCAAATTAACAGAGTTATGAATTTGCCAAAGACAGCTGGCCATAGTT 180

Qy 481 TCGCAAAATGTTGAGCTTTTCATAATTCAGAGCTTTTAAATCGACGATATAGAAGATAAT 540
Db 181 TCGCAAAATGTTGAGCTTTTCATAATTCAGAGCTTTTAAATCGACGATATAGAAGATAAT 240

Qy 541 GCTCCCTTGAGAGGGGACAGACCACTTCTCACTTAATCTCGGTGTACCTCCACTATA 600
Db 241 GCTCCCTTGAGAGGGGACAGACCACTTCTCACTTAATCTCGGTGTACCTCCACTATA 300

Qy 601 AACACCGCAATATATATGTTTTCAGAGCCATGCACTGTATCGCAGCTAACCAAAA 660
Db 301 AACACCGCAATATATATGTTTTCAGAGCCATGCACTGTATCGCAGCTAACCAAAA 360

Qy 661 GAGCCTTTGATCATAATTTGATPACGATTTTCAACGAAGAATGATCAATCTACATAGG 720
Db 361 GAGCCTTTGATCATAATTTGATPACGATTTTCAACGAAGAATGATCAATCTACATAGG 420

Qy 721 GGACAGGCTTGGATATATATCTGAGAGACTTTCTGCTGAATCATACCTACTCAGGAG 780
Db 421 GGACAGGCTTGGATATATATCTGAGAGACTTTCTGCTGAATCATACCTACTCAGGAG 480

Qy 781 ATGATTTTGAATATGGTTATGATAAACAAGGGGCGCTTTTCAGATTAAGCTTGAGACTC 840
Db 481 ATGATTTTGAATATGGTTATGATAAACAAGGGGCGCTTTTCAGATTAAGCTTGAGACTC 540

Qy 841 ATGGAAGCGCTGTCTCTCTCCATCAGCAGCGGCAATTCGTTGGTTCCTTTTCAATAATCTT 900
Db 541 ATGGAAGCGCTGTCTCTCTCCATCAGCAGCGGCAATTCGTTGGTTCCTTTTCAATAATCTT 600

Qy 901 CTGGGTATTTATCAGATTAGATGATGATTAATGAAATTTGAAAGATTTCCAAATGTCC 960
Db 601 CTGGGTATTTATCAGATTAGATGATGATTAATGAAATTTGAAAGATTTCCAAATGTCC 660

Qy 961 AGCGAAAAGCGCTTTCGTGAGGACATTAACAGAGGGGAGTTATCTTTTCCCATGCTCCAC 1020
Db 661 AGCGAAAAGCGCTTTCGTGAGGACATTAACAGAGGGGAGTTATCTTTTCCCATGCTCCAC 720

Qy 1021 GCCCTTAACTTCACTAAAACGAAGGTCAAACTGAGCAACAATGAAATTTCTAAGAAAT 1080
Db 721 GCCCTTAACTTCACTAAAACGAAGGTCAAACTGAGCAACAATGAAATTTCTAAGAAAT 780

Qy 1081 CTCTGTGTGAGGACAAAGTATAAGATATAAATACTAAGCTGATTTCAATCTGGAATTC 1140
Db 781 CTCTGTGTGAGGACAAAGTATAAGATATAAATACTAAGCTGATTTCAATCTGGAATTC 840

Qy 1141 GACACCAATTCNTGGGCTACACCAAAATTTTATTAATCAATAGTGAATATGATAAAA 1200
Db 841 GACACCAATTCNTGGGCTACACCAAAATTTTATTAATCAATAGTGAATATGATAAAA 900

Qy 1201 AATGATATGAAATAAGTATTTACCTGATTTGGCTTTCGATTTCCGATTCGACCGCCACCAAT 1260
Db 901 AATGATATGAAATAAGTATTTACCTGATTTGGCTTTCGATTTCCGATTCGACCGCCACCAAT 658

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Db 901 AATGATAAATGAAAAAATAGTATTACCTGATTTGGCTTCGCATCCGACACCGCCACCAAT 960
Qy 1261 TTACATGACGAATTTGTATATATAATAGACCACTTTATCCGAATG 1305
Db 961 TTACATGACGAATTTGTATATATAATAGACCACTTTATCCGAATG 1005

RESULT 3
US-08-469-665-1
; Sequence 1, Application US/08469665
; Patent No. 5786193
; GENERAL INFORMATION:
; APPLICANT: GREENE, ET AL.
; TITLE OF INVENTION: Human Geranylgeranyl Pyrophosphate Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,665
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00421
; FILING DATE: 11 JAN 95
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-377
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
; US-08-469-665-1

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Query Match      7.3%; Score 114; DB 2; Length 903;
Best Local Similarity 52.1%; Pred. No. 2.9e-19;
Matches 348; Conservative 0; Mismatches 290; Indels 30; Gaps 3;

Qy 359 AAAGCTTGATTTCCAAACCTTATAATCACATCTCTTTTGAACCTGGCAAGACTTTAGAC 418
Db 26 AAAGAAATCTTCTAGAACCTTATAATATCTTCTAGTTACCAGGTAACAGATGAGAA 85

Qy 419 TAAATTTAATAGTTCAAATTAACAGAGTTATGAATTTGCCCAAGACCCAGCTGGCCATAG 478
Db 86 CCAAACTTTCCAGAGCATTTAATCAATTTGGCTGAAAGTTCCAGAGGACAAGCTACAGATTA 145

Qy 479 TTTCCGAAATTTGTAGCTCTTTCGATTAATTCAGACCTTTTAAATCGACGATATAGAAGATA 538
Db 146 TTATTGAAGTGACAGAAATGTTGCATAATGCCAGTTTACTCATCGATGATATTGAAGACA 205

Qy 539 ATGCTCCCTTGAGAGGGGACAGACCACTTCTCACTTAATCTTCGGTGTACCTCCACTA 598
Db 206 ACTCAAAACTCCGACGCTGGCTTTCCAGTGGCCCAAGCATCTATGGAAATCCCATCTGTCA 265

Qy 599 TAAACACCGCAAAATTTATATGTTATTTTCAGAGCCCATGCAACTTGTATCGCAGCTAACCAA 658

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Db      266 TCAATCTGCCAATAGGTGATTTCTTGGCTTGGAGAAAGTCT----- 310
QY      659 AAGAGCCTTTGATCATATAATTTGATTAACGATTTTCAACGAAGAATTTGATCAATCTACATA 718
Db      311 TAACCTCTTGATCACCCAGATGCAGTGAAGCTTTTACCCGCCAGCTTTTGGAACTCCATC 370
QY      719 GGGGCAAGCCTTGGATATATATCTGAGAGACTTTCTGCTGAAATCATACCTACTCAGG 778
Db      371 AGGGCAAGCCTTAGATATTTACTGGAGGA-----TAATTACACTTGTCCCACTGAAG 424
QY      779 AGATGATTTTGAATATGGTTATGAATAAACAAGCGGCTTTTTCAGATTAACGTTGAGAC 838
Db      425 AGAATATTAAGCTATGGTCTGCAGAAAACAGTGGACTTTTGGATTTAGCAGTAGGTC 484
QY      839 TCATGAAGCGCTGCTCTCTCTCTCAACACCGGCCCAATTCGTTGGTCTCTTTTCATATAATC 898
Db      485 TCATGACGTTGTTCTCTGATTAACAAGAATTTAAACCGCTACTT-----AATA 535
QY      899 TTCTGGGTATTTATTCAGATTAGAGATGATTAATCTTGAAGATTTCCAAATGT 958
Db      536 CACTTGGGCTCTTTTCCAAATTAGGATGATTAATCTTGAAGATTTCCAAAGATATA 595
QY      959 CCAGCGAAAAGCCTTTGCTGAGGACATTAACAGAGGGAGTTATCTTTTCCCATCGTCC 1018
Db      596 GTGAAAACAAAAGTTTGGGTGAAGATCTGACAGAGGGAAGTTCTCATTTCTACTATTTC 655
QY      1019 ACGCCCTT 1026
Db      656 ATGCTATT 663

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RESULT 4

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US-09-038-596-1
; Sequence 1, Application US/09038596
; Patent No. 5928924
; GENERAL INFORMATION:
; APPLICANT: GREENE, ET AL.
; TITLE OF INVENTION: Human Geranylgeranyl Pyrophosphate Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,596
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,665
; FILING DATE: June 6, 1995
; APPLICATION NUMBER: PCT/US95/00421
; FILING DATE: 11 JAN 95
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-377
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE

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; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
US-09-038-596-1

Query Match      7.3%; Score 114; DB 2; Length 903;
Best Local Similarity 52.1%; Pred. No. 2,9e-19;
Matches 348; Conservative 0; Mismatches 290; Indels 30; Gaps 3;

QY      359 AAAGCTTGATTTCAAAAACCTTATAATCAATCCTTTTGAACCTGCGCAAGAACTTTAGAC 418
Db      26  AAAGAATTTCTTAGAACCTTATAATCAATCTTACTTCACTTACAGGTAACAAGTCAGAA 85
QY      419 TAAATTTAATAGTTCAAAATTAACAGAGTTATGAATTTGCCAAGACCCAGCTGGCCATAG 478
Db      86  CCAAACTTTCAAGGCAATTTAATCAATTTGGCTGAAAGTTCCAGAGGCAAGCTACAGATTA 145
QY      479 TTTTCGCAAAATTTGTGAGCTCTTTGCATAAATTCAGAGCCCTTTTAAATCGACGATATAGAAGATA 538
Db      146 TTATTGAGTGCAGAGAAATGTTGCATTAATGCCAGTTTACTCATCGATGATATTGAAGACA 205
QY      539 ATGCTCCCTTGAAGAGGGGACAGACCACTTCTCACTTAATCTTTCGGTGTACCCCTCCACTA 598
Db      206 ACTCAAAACTCCGAGCTGGCTTTCCAGTGGCCCAACAGCATCTATGGAATCCCATCTGTCA 265
QY      599 TAAACACCCCAATTTATATGATTTTTCAGAGCCCATGCAACTTGTATCCAGCTAACCCACA 658
Db      266 TCAATTTCTGCCAAATTAACGTTATTTCTTGGCTTGGAGAAAGTCT----- 310
QY      659 AAGAGCCTTTGATCATATAATTTGATTAACGATTTTCAACGAAGAATTTGATCAATCTACATA 718
Db      311 TAACCTCTTGATCACCCAGATGCAGTCAAGCTTTTACCCGCCAGCTTTTGGAACTCCATC 370
QY      719 GGGGCAAGCCTTGGATATATATCTGAGAGACTTTTCTGCTGAAATCATACCTACTCAGG 778
Db      371 AGGGCAAGGCTCTAGATATTTACTCGAGGGA-----TAATTACACTTGTGCCCACTGAAG 424
QY      779 AGATGATTTTGAATATGGTTATGAATAAACAAGGGCGCTTTTTCAGATTAACGTTGAGAC 838
Db      425 AGAATATAAAGCTATGGTCTGCAGAAAACAGGTTGAGTCTTTGGATTTAGCAGTAGGTC 484
QY      839 TCATGAAGCGCTGCTCTCTCTCTCAACACCGGCCCAATTCGTTGGTCTCTTTTCATATAATC 898
Db      485 TCATGACGTTGTTCTCTGATTAACAAGAATTTAAACCGCTACTT-----AATA 535
QY      899 TTCTGGGTATTTATTCAGATTAGAGATGATTAATCTTGAAGATTTGAAGATTTCCAAATGT 958
Db      536 CACTTGGGCTCTTTTCCAAATTAGGATGATTAATCTTGAAGATTTCCAAAGATATA 595
QY      959 CCAGCGAAAAGCCTTTGCTGAGGACATTAACAGAGGGAGTTATCTTTTCCCATCGTCC 1018
Db      596 GTGAAAACAAAAGTTTGGGTGAAGATCTGACAGAGGGAAGTTCTCATTTCTACTATTTC 655
QY      1019 ACGCCCTT 1026
Db      656 ATGCTATT 663

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RESULT 5

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PCT-US95-00421-1
; Sequence 1, Application PC/TUS9500421
; GENERAL INFORMATION:
; APPLICANT: GREENE, ET AL.
; TITLE OF INVENTION: Human Geranylgeranyl Pyrophosphate Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:

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[illegible]

RESULT 7

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US-09-248-796A-3882
; Sequence 3882, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 3882
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-3882

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Query Match	4.18;	Score 65;	DB 3;	Length 498;
Best Local Similarity	58.8;	Pred. No. 7.4e-07;		
Matches 151;	Conservative 0;	Mismatches 100;	Indels 6;	Gaps 2;

Qy	784	TATTTGAATATGTTATGAATAAAACAGCGGGCCCTTTTCAGATTAAAGCTTGAGACTCATG	843
Db	10	TATTTGAAATGATTAAAGATAAAACTGGTGGTGTGTTTCAGATTGGCAATCAAATATTATG	69
Qy	844	GAAGCGCTGTCTCCTTCCTCACACCGGCCCATTCGTTGGTTCCTTTTCATAAATCTTCCTG	903
Db	70	CTGTTGTTATTCAGATGTACAGAAAACG---ATCAATTAATATCCCTTGCAAATTTAATG	126
Qy	904	GGTATTATTTATCAGATTAGAGATGATTACTTGAATTTGAAAGATTTCCAAATGTCACGC	963
Db	127	GGCATTTTGTATCAAGTTTAGAGACGATATTTTGAATTTAGTGGATGCCAAGTATTTCTGCG	186
Qy	964	GAATAAGGCTTTGC---TGAGGCATTTACAGAGGGGAAGTTATCTTTTCCCATCGTCCAC	1020
Db	187	ATGAAGGCGACTACATGTGAAGACTTGTATAGAGGGAAGTTATCATTTGCCTATTATTACAT	246
Qy	1021	GCCCTTAACTTCACTAA	1037
Db	247	TGTCGAAGAACCACTAA	263

RESULT 8

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US-09-621-976-2813/c
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET-054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335

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; SOFTWARE: Patent.pm
; SEQ ID NO 2813
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; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

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Query Match	3.4%;	Score 52.6;	DB 3;	Length 832;
Best Local Similarity	16.0%;	Pred.No. 0.0013;		
Matches	45;	Conservative 133;	Mismatches 102;	Indels 1; Gaps 1;
Qy	1268	ACGAATTGTTATATATATAGACCACTTATCCGAANTGTGGAATAATAAATGATCAATCAAA	1327	
Db	393	AAGAATTGTACCAATAAATAATATATATTTGTYTWWTKTWYWTYTTT:MMWKKKARR	334	
Qy	1328	TTAGTCGAGGAATAGTCAGAAATAA-AGCCTTCCTCTCCTCTCTTCGCATCTATACA	1386	
Db	333	WYTWKSTYACGRYKTYTGMWYWKRMWSTRWYCMKWKCMYGRGRRCAYTWWGR	274	
Qy	1387	TACGATTTTCATATATACGTTTTCATCGATCACTTTTGTATATATCTCAAAAAGATCTTT	1446	
Db	273	MWSYAMGWKWSMRSMCMCTRMYYKKGSGTYWTKCTCATCYWYWKYKRMWSKTCWSGS	214	
Qy	1447	AGTTCCCAATAGTCAAACTCTCCAAATTTATATAGCCTTTTATATTTTTCACAGATTCTGA	1506	
Db	213	RGGYMSYTSRYSWYKASWMTYCMWGRWWSWTWYMWAGKKWRYATWTRRMMW	154	
Qy	1507	AATCCCTTTTATCAGACCGTTTAATCTAGCGGTTACTGT	1547	
Db	153	AANTMMYMWAMCMSRGAAMYRTTMMWMMGYVYWRKESY	113	

RESULT 9

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US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAEL promoters
US-09-806-708B-22

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	Query Match	3.2%	Score 49.8;	DB 3;	Length 1141;
	Best Local Similarity	12.7%;	Pred. No. 0.0074;		
	Matches	97;	Conservative 257;	Mismatches 408;	Indels 2; Gaps 2;
Qy	295	AAATCAATGAGGCCAAGATAGATGACTGCATCAATAATCATCTCTTTGGTCCAGCAA	354		
	:	:: :::	: : :	: : : :::	: : :
Dd	377	WHANAHSRKWTBYVKRTMVNNNGTTWKKRWAWYKWDMDWBCTYNNNNNGRYY	436		
Qy	355	AATGAAGCTTGATTTCAAAACCTTAATATCATCCTCTTTGAAACCTGCAGAAGCTTT	414		
	:	: :	: : :	: : : :::	: : :
Dd	437	GWTKNKGWTTYKWKANNCKWRADHKTCTHNNTTWKMKTYWNNCYKSSMTNGKSRBA	496		
Qy	415	AGACTAAATTAATAGTTTCAAAATTAACAGAGTTATGNAATTTGCCAAGACCAGCTGCC	474		
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5 LOCATION: (94812)..(84812)
6 OTHER INFORMATION: n equals a, t, c, or g
7 NAME/KEY: misc_feature
8 LOCATION: (98120)..(98120)
9 OTHER INFORMATION: n equals a, t, c, or g
10 NAME/KEY: misc_feature
11 LOCATION: (98159)..(98159)
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62 LOCATION: (319226)..(319226)
63 OTHER INFORMATION: n equals a, t, c, or g
64 NAME/KEY: misc_feature
65 LOCATION: (559167)..(559167)
66 OTHER INFORMATION: n equals a, t, c, or g
67 NAME/KEY: misc_feature
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69 OTHER INFORMATION: n equals a, t, c, or g
70 NAME/KEY: misc_feature
71 LOCATION: (1600992)..(1600992)
72 OTHER INFORMATION: n equals a, t, c, or g
73 NAME/KEY: misc_feature

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; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (657203)..(657203)
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; NAME/KEY: misc.feature
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; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g
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; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
Query Match 3.1%; Score 48.2; DB 3; Length 1664976;
Best Local Similarity 48.1%; Pred. No. 0.25;
Matches 137; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 368 TTTCAAAACCTTATATACATCCTTTTGAACCTGGCGAAGAACTTTAGACTAAATTTAA 427
Db 688622 TATATAACCGTCAAAACATCTTCTATTGCTGGAGAAAGAAATTAGCCATATTTAA 688681

QY 428 TAGTTCAATTAACAGAGTTATGAATTTGCCAAAGACCAGCTGGCCATGTTTCGCAA 487
Db 688682 CTGTAGTAACCTTATATGTTGAAGAAAGACGATATTGAGGAGGTTTTCAGCGCGCTG 688741

QY 488 TTGTTGAGCTCTTGCAATATCCAGCCTTTTAAATCGACGATATAGAAGATAATGCTCCCT 547
Db 688742 CAGTAGAGTTAATTCACAACTACACCTTAATACATGATGACATATTGGACAATGATG 688801

QY 548 TGAGAAGGGGACAGACCCTTCTCACTTAATCTTGGTGTACCTCCACTATAAACACCG 607
Db 688802 AGAGGAGAGGAAACCAACAGTTTCATGTTGCTATGGAGAGCAATGGCTATCTTAGCTG 688861

QY 608 CAAATTATATGTTATTCAGAGCCATGCAACTTGTATCGCAGCTAA 652
Db 688862 GAGATTTATTATATGCTAAAGCTTTTGAAGCAGTTTCAAGAAATAA 688906

RESULT 11
US-09-692-570-1
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6797466
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
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; NAME/KEY: misc feature
; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (1313224)..(1313224)
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n equals a, t, c, or g

Query Match          3.1%; Score 48.2; DB 3; Length 1664976;
Best Local Similarity 48.1%; Pred. No. 0.25;
Matches 137; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 368 TTTCAAAACCTTATAATCATCATCTTTTGAAACCTGCGCAAGAACTTTAGACTAAATTTAA 427
Db 688622 TATATAACGGCTCAAAACATCTTCTATTGCTGGAGAAAGAAATTAGGCCATATTTAA 688681

QY 428 TAGTTCAAATTAAACAGAGTTATGAATTTGCCAAAGACCAGCTGGCCATAGTTTCGCAAA 487
Db 688682 CTCTAGTAACTTATATGTTGAAGAAAGACGATATTGAGGAGGTTTTCGCCAGCGCTG 688741

QY 488 TTGTTGAGCTCTTGCAATATTCAGCGCTTTTAAATCGACGATATAGAAATATGCTCCCT 547
Db 688742 CAGTAGAGTTAATTCACAACTACACCTTAATACATGATGACATATATGGAATGATG 688801

QY 548 TGAGAAGGGGACAGACACTTCTCACTTAATCTTCGCTGTACCTCCACTATAAACAACCG 607
Db 688802 AGAGGAGAGGAAACCAACAGTTCATGTTCTATGAGAGGCAATGGCTATCTTAGCTG 688861

QY 608 CAAATTATATGTTATTTTCAGAGCCATGCAACTGTTATCGCAGCTAA 652
Db 688862 GAGATTTATTATATGCTTAAAGCTTTTGAAGCAGTTTCAAGNATAA 688906

RESULT 12
US-10-027-983-11
; Sequence 11, Application US/10027983
; Patent No. 661762
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Mark P. Roach
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
; FILE REFERENCE: RTS-0340
; CURRENT APPLICATION NUMBER: US/10/027,983
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 11
; LENGTH: 392000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 137740
; OTHER INFORMATION: unknown
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; LOCATION: 137742
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; OTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: exon 5:intron 5
; NAME/KEY: exon:intron junction
; LOCATION: (299248)..(299249)
; OTHER INFORMATION: exon 9:intron 9
; NAME/KEY: exon:intron junction
; LOCATION: (348578)..(348579)
; OTHER INFORMATION: exon 10:intron 10
; NAME/KEY: intron
; LOCATION: (348579)..(381838)
; OTHER INFORMATION: intron 10
; NAME/KEY: intron:exon junction
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; OTHER INFORMATION: intron 11:exon 12
; US-10-027-983-11
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Query Match 2.9%; Score 45.2; DB 3; Length 392000;
Best Local Similarity 50.0%; Pred. No. 0.86;
Matches 113; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

Query Match	2.8%	Score 44.6;	DB 3;	Length 50000;
Best Local Similarity	45.9%;	Pred. NO. 0.6;		
Matches 152;	Conservative	0;	Mismatches 179;	Indels 0;
Gaps	0;			

Query Match	2.8%;	Score 44.6;	DB 3;	Length 50000;
Best Local Similarity	45.9%;	Pred. No. 0.6;		
Matches 152;	Conservative 0;	Mismatches 179;	Indels 0;	Gaps 0;
Qy	1096	AGTGATTAAGATATATAAACTGAAGCTGATTCAAATCTGGAATTCGACACCAATTCATTG	1155	
Db	25864	AATCTTAAACCTTATTATACCAATAAAATTTATCATAAATGATAAAGAAATAGAAATTAAT	25805	
Qy	1156	GCCTACACCAAAAATTTTATTAAATCAATTAGTGAATATGATAAAAAATGATAATGAAAAAT	1215	
Db	25804	GAAATTAAGAAAAATAACTATATTCTAGATGAATATATAAAAAATATAATTTTAAA	25745	
Qy	1216	AGATATTTACCTGATTTGGCTTCGCAATCCGACACGCCACCAATTTACATGACGAATTG	1275	
Db	25744	ATATCTAGATAGAATTTAAATAAAAATAAAATATAGATAATATTAAACAAAATCAAAATTA	25685	
Qy	1276	TTATATATATAGACCACTTATCCGAATTTGGAATAAATTTGATCAATCAAAATTAGTGG	1335	
Db	25684	TGGGATTTATTTAAGCAATATNTTGGATGGAAAAATAGTAAACACCTATATAATTTATAAT	25625	
Qy	1336	GGAAGATAGTCGAAATAAGCGTTCTCTCTCCCTCTTTTGGCATCTATACATACGATTTTC	1395	
Db	25624	GATAAAAAATTAACATAACTATTATGATTAATATAGTTTTTTTTCATATGCTAACATTTTA	25565	
Qy	1396	ATATATACGTTTCATTTGCATCATCTTTTGGAT	1426	
Db	25564	GTATATTTTTCTAACTTAATTTACTTTCATCAT	25534	

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RESULT 15
US-09-806-708B-23/c
; Sequence 23, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 1055

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; FEATURES:
; NAME/KEY: promoter
; LOCATION: (1)..(1055)
; OTHER INFORMATION: consensus sequence of A.t. and L.a. FAEI promoters
US-09-806-708B-23

Query Match          2.7%; Score 43; DB 3; Length 1055;
Best Local Similarity 21.2%; Pred No. 0.39;
Matches 126; Conservative 157; Mismatches 299; Indels 12; Gaps 2;

Qy      886  CCTTTCATAAATCTTCTGGGTATTATTATCATGATAGAGATGATCTTGAATTTGAAA  945
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Db      634  CATNTTWAATNTTTRAGRGAAATKTGTTSTTAGWMTGTGATTCGNNNNNNNNNNCMTASC  575

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